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10/018470

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-key terms

L1 107 SEA FILE=CAPLUS ABB=ON PLU=ON (ORF OR OPEN READ? FRAME OR PROTEIN CODING SEQUENC?)(L)(NMB OR (NEISSER? OR N)(W)MENINGITID? OR MENINGOCOCC?)
L2 71 SEA FILE=CAPLUS ABB=ON PLU=ON L1(L)(IDENTIF? OR DETERM? OR DETECT? OR DET## OR SCREEN?)
L3 24 SEA FILE=CAPLUS ABB=ON PLU=ON L2(L)NUCLEOTIDE
L4 22 SEA FILE=CAPLUS ABB=ON PLU=ON L3(L)(AMINO OR PROTEIN OR POLYPROTEIN OR PEPTIDE OR POLYPEPTIDE)

L4 ANSWER 1 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 05 Apr 2001
ACCESSION NUMBER: 2001:240640 CAPLUS
DOCUMENT NUMBER: 135:2651
TITLE: Mu-like prophage in serogroup B Neisseria meningitidis coding for surface-exposed antigens
AUTHOR(S): Masignani, Vega; Giuliani, Marzia Monica; Tettelin, Herve; Comanducci, Maurizio; Rappuoli, Rino; Scarlato, Vincenzo
CORPORATE SOURCE: Department of Molecular Biology, IRIS, Chiron S.p.A., Siena, 53100, Italy
SOURCE: Infection and Immunity (2001), 69(4), 2580-2588
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Sequence anal. of the genome of N. meningititidis serogroup B revealed the presence of an .apprx.35-kb region inserted within a putative gene coding for an ABC-type transporter. The region contains 46 **open reading frames**, 29 of which are colinear and homologous to the genes of Escherichia coli Mu phage. Two prophages with similar organizations were also found in serogroup A **meningococcus**, and one was found in Haemophilus influenzae. Early and late phage functions are well preserved in this family of Mu-like prophages. Several regions of atypical **nucleotide** content were **identified**. These likely

represent genes acquired by horizontal transfer. Three of the acquired genes are shown to code for surface-associated antigens, and the encoded **proteins** are able to induce bactericidal antibodies.
REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 28 Mar 2001
ACCESSION NUMBER: 2001:215888 CAPLUS
DOCUMENT NUMBER: 135:222148
TITLE: Exl, an exchangeable genetic island in Neisseria meningitidis
AUTHOR(S): Kahler, C. M.; Blum, E.; Miller, Y. K.; Ryan, D.; Popovic, T.; Stephens, D. S.
CORPORATE SOURCE: Department of Medicine and Department of Microbiology and Immunology, Emory University School of Medicine, Atlanta, GA, USA
SOURCE: Infection and Immunity (2001), 69(3), 1687-1696
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The genetic structure and evolution of a novel exchangeable **meningococcal** genomic island was defined for the important human pathogen **Neisseria meningitidis**. In 125 **meningococcal** strains tested, one of three unrelated **nucleotide** sequences, designated exl (exchangeable locus), was found between a gene required for heme utilization, hemO, and col, encoding a putative Escherichia coli collagenase homolog. The 5' boundary of each exl cassette was the stop codon of hemO, whereas the 3' boundary was delineated by a 33-bp repeat containing neisserial uptake sequences located downstream of col. One of the three alternative exl cassettes contained the **meningococcal** Hb receptor gene, hmbR (exl3). In other **meningococcal** strains, hmbR was absent from the genome and was replaced by either a **nucleotide** sequence containing a novel **open reading frame**, exl2, or a cassette containing exl3. The **proteins** encoded by exl2 and exl3 had no significant **amino** acid homol. to HmbR but contained six motifs that are also present in the lipoprotein components of the lactoferrin (LbpB), transferrin (TbpB), and Hb-haptoglobin (HpuA) uptake systems. To **determine** the evolutionary relationships among **meningococci** carrying hmbR, exl2, or exl3, isolates representing 92 electrophoretic types were examined HmbR was found throughout the population structure of **N. meningitidis** (genetic distance, >0.425), whereas exl2 and exl3 were found in clonal groups at genetic distances of <0.2. The commensal neisserial species were **identified** as reservoirs for all of the exl cassettes found in **meningococci**. The structure of these cassettes and their correlation with clonal groups emphasize the extensive gene pool and frequent horizontal DNA transfer events that contribute to the evolution and virulence of **N. meningitidis**.
REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 08 Jun 1999

ACCESSION NUMBER: 1999:350393 CAPLUS
DOCUMENT NUMBER: 131:156678
TITLE: Antigenic and molecular conservation of the gonococcal NspA protein
AUTHOR(S): Plante, Martin; Cadieux, Nathalie; Rioux, Clement R.; Hamel, Josee; Brodeur, Bernard R.; Martin, Denis
CORPORATE SOURCE: Unite de Recherche en Vaccinologie, Centre Hospitalier Universitaire de Quebec et Universite Laval, Ste-Foy, QC, G1V 4G2, Can.
SOURCE: Infection and Immunity (1999), 67(6), 2855-2861
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A low-mol.-weight **protein** named NspA (neisserial surface **protein** A) was recently **identified** in the outer membrane of all **Neisseria meningitidis** strains tested. Antibodies directed against this **protein** were shown to protect mice against an exptl. **meningococcal** infection. Hybridization expts. clearly demonstrated that the nspA gene was also present in the genomes of the 15 Neisseria gonorrhoeae strains tested. Cloning and sequencing of the nspA gene of N. gonorrhoeae B2 revealed an **open reading frame** of 525 **nucleotides** coding for a **polypeptide** of 174 **amino** acid residues, with a calculated mol. weight of 18,316 and a pI of 10.21. Comparison of the predicted **amino** acid sequence of the NspA **polypeptides** from the gonococcal strains B2 and FA1090, together with that of the **meningococcal** strain 608B, revealed an identity of 93%, suggesting that the NspA **protein** is highly conserved among pathogenic Neisseria strains. The level of identity rose to 98% when only the two gonococcal predicted NspA **polypeptides** were compared. To evaluate the level of antigenic conservation of the gonococcal NspA **protein**, monoclonal antibodies (MAbs) were generated. Four of the seven NspA-specific MAbs described in this report recognized their corresponding epitope in 100% of the 51 N. gonorrhoeae strains tested. Radioimmunobinding assays clearly indicated that the gonococcal NspA **protein** is exposed at the surface of intact cells.
REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 06 Aug 1998
ACCESSION NUMBER: 1998:489158 CAPLUS
DOCUMENT NUMBER: 129:227136
TITLE: Structure and function of repetitive sequence elements associated with a highly polymorphic domain of the Neisseria meningitidis PilQ protein
AUTHOR(S): Tonjum, Tone; Caugant, Dominique A.; Dunham, Steve A.; Koomey, Michael
CORPORATE SOURCE: Section of Molecular Microbiology, National Hospital, Institute of Microbiology, Oslo, N-0027, Norway
SOURCE: Molecular Microbiology (1998), 29(1), 111-124
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal

LANGUAGE: English

AB Secretins are a large family of **proteins** associated with membrane translocation of macromol. complexes, and a subset of this family, termed PilQ **proteins**, is required for type IV pilus biogenesis. The authors analyzed the status of PilQ expression in **Neisseria meningitidis** (Mc) and found that PilQ- mutants were non-piliated and deficient in the expression of pilus-associated phenotypes. Sequence anal. of the 5' portion of the pilQ **ORF** of the serogroup B Mc strain 44/76 showed the presence of seven copies of a repetitive sequence element, in contrast to the situation in N. gonorrhoeae (Gc) strains, which carry either two or three copies of the repeat. The derived **amino** acid sequence of the consensus **nucleotide** repeat was an octapeptide PAKQQAAA, designated as the small basic repeat (SBR). This gene segment was studied in more detail in a collection of 52 Mc strains of diverse origin by **screening** for variability in the size of the PCR-generated DNA fragments spanning the SBRs. These strains were found to harbor from four to seven copies of the repetitive element. No association between the number of copies and the serogroup, geog. origin or multilocus genotype of the strains was evident. The presence of polymorphic repeat elements in Mc PilQ is unprecedented within the secretin family. To address the potential function of the repeat containing domain, Mc strains were constructed so as to express chimeric PilQ mols. in which the number of SBR repeats was increased or in which the repeat containing domain was replaced in toto by the corresponding region of the Pseudomonas aeruginosa (Pa) PilQ **protein**. Although the strain expressing PilQ with an increased number of SBRs was identical to the parent strain in pilus phenotypes, a strain expressing PiIQ with the equivalent Pa domain had an eightfold reduction in pilus expression level. The findings suggest that the repeat containing domain of PilQ influences Mc pilus expression quant. but not qual.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN

ED Entered STN: 25 Mar 1998

ACCESSION NUMBER: 1998:174432 CAPLUS

DOCUMENT NUMBER: 128:304595

TITLE: Characterization of the gene cassette required for biosynthesis of the (α1→6)-linked N-acetyl-D-mannosamine-1-phosphate capsule of serogroup A Neisseria meningitidis

AUTHOR(S): Swartley, John S.; Liu, Li-Jun; Miller, Yoon K.; Martin, Larry E.; Edupuganti, Srilatha; Stephens, David S.

CORPORATE SOURCE: Department of Medicine, Emory University School of Medicine, Atlanta, GA, 30303, USA

SOURCE: Journal of Bacteriology (1998), 180(6), 1533-1539 CODEN: JOBAAY; ISSN: 0021-9193

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The (α1→6)-linked N-acetyl-D-mannosamine-1-phosphate **meningococcal** capsule of serogroup A **Neisseria meningitidis** is biochem. distinct from the sialic acid-containing capsules produced by other disease-associated **meningococcal** serogroups (e.g., B, C, Y, and W-135). We defined the genetic

cassette responsible for expression of the serogroup A capsule. The cassette comprised a 4,701-bp **nucleotide** sequence located between the outer membrane capsule transporter gene, ctrA, and galE, encoding the UDP-glucose-4-epimerase. Four **open reading frames** (**ORFs**) not found in the genomes of the other **meningococcal** serogroups were **identified**. The first serogroup A **ORF** was separated from ctrA by a 218-bp intergenic region. Reverse transcriptase (RT) PCR and primer extension studies of serogroup A mRNA showed that all four **ORFs** were cotranscribed in the opposite orientation to ctrA and that transcription of the **ORFs** was initiated from the intergenic region by a σ-70-type promoter that overlapped the ctrA promoter. The first **ORF** exhibited 58% **amino** acid identity with the UDP-N-acetyl-D-glucosamine (UDP-GlcNAc) 2-epimerase of Escherichia coli, which is responsible for the conversion of UDP-GlcNAc into UDP-N-acetyl-D-mannosamine. Polar or nonpolar mutagenesis of each of the **ORFs** resulted in an abrogation of serogroup A capsule production as **determined** by colony immunoblots and ELISA. Replacement of the serogroup A biosynthetic gene cassette with a serogroup B cassette by transformation resulted in capsule switching from a serogroup A capsule to a serogroup B capsule. These data indicate that assembly of the serogroup A capsule likely begins with monomeric UDP-GlcNAc and requires **proteins** encoded by three other genes found in the serogroup A **N. meningitidis**-specific operon located between ctrA and galE.

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 6 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Feb 1998
ACCESSION NUMBER: 1998:84265 CAPLUS
DOCUMENT NUMBER: 128:202792
TITLE: Molecular characterization of LbpB, the second lactoferrin-binding protein of Neisseria meningitidis
AUTHOR(S): Pettersson, Annika; Prinz, Thorsten; Umar, Arzu; Van Der Biezen, Jenny; Tommassen, Jan
CORPORATE SOURCE: Department of Molecular Cell Biology and Institute of Biomembranes, Utrecht University, Utrecht, 3584 CH, Neth.
SOURCE: Molecular Microbiology (1998), 27(3), 599-610
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The lbpA gene of **Neisseria meningitidis** encodes an outer membrane lactoferrin-binding **protein** and shows homol. to the transferrin-binding **protein**, TbpA. Previously, we have **detected** part of an **open reading frame** upstream of lbpA. The putative product of this **open reading frame**, tentatively designated lbpB, showed homol. to the transferrin-binding **protein** TbpB, suggesting that the lactoferrin receptor, like the transferrin receptor, consists of two **proteins**. The complete **nucleotide** sequence of lbpB was **determined** The gene encodes a 77.5 kDa **protein**, probably a lipoprotein, with homol., 33% identity to the TbpB of **N. meningitidis** . A unique feature of LbpB is the presence of two stretches of neg.

charged residues, which might be involved in lactoferrin binding. Antisera were raised against synthetic **peptides** corresponding to the C-terminal part of the putative **protein** and used to demonstrate that the gene is indeed expressed. Consistent with the presence of a putative Fur binding site upstream of the lbpB gene, expression of both LbpA and LbpB was proved to be iron regulated in Western blot expts. The LbpB **protein** appeared to be less stable than TbpB in SDS-containing sample buffer. Isogenic mutants lacking either LbpA or LbpB exhibited a reduced ability to bind lactoferrin. In contrast to the lbpB mutant, the lbpA mutant was completely unable to use lactoferrin as a sole source of iron.

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 7 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 05 Jun 1997
ACCESSION NUMBER: 1997:352039 CAPLUS
DOCUMENT NUMBER: 127:61399
TITLE: Identification and characterization of a DNA region involved in the export of capsular polysaccharide by Actinobacillus pleuropneumoniae serotype 5a
AUTHOR(S): Ward, Christine K.; Inzana, Thomas J.
CORPORATE SOURCE: Center Molecular Medicine Infectious Diseases, Virginia-Maryland Reginal College Veterinary Medicine, Virginia Polytechnic Institute and State University, Blacksburg, VA, 24061-0342, USA
SOURCE: Infection and Immunity (1997), 65(6), 2491-2496
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Actinobacillus pleuropneumoniae synthesizes a serotype-specific capsular polysaccharide that acts as a protective barrier to phagocytosis nd complement-mediated killing. To begin understanding the role of A. pleuropneumoniae capsule in virulence, the authors sought to **identify** the genes involved in capsular polysaccharide export and biosynthesis. A 5.3-kb XbaI fragment of A. pleuropneumoniae serotype 5a J45 genomic DNA that hybridized with DNA probes specific for the Haemophilus influenzae type b cap export region was cloned and sequenced. This A. pleuropneumoniae DNA fragment encoded four **open reading frames**, designated cpxDCBA. The **nucleotide** and predicted **amino** acid sequences of cpxDCBA contained a high degree of homol. to the capsule export genes of H. influenzae type b bexDCBA, **Neisseria meningitidis** group B ctrABCD, and, to a lesser extent, Escherichia coli K1 and K5 kpsE and kpsMT. When present in trans, the cpxDCBA gene cluster complemented kpsM::TnphoA or kpsT::TnphoA mutations, **determined** by enzyme immunoassay and by restored sensitivity too a K5-specific bacteriophage. A cpxCB probe hybridized to genomic DNA from all A. pleuropneumoniae serotypes tested, indicating that this DNA was conserved among serotypes. These data suggest that A. pleuropneumoniae produces a group II family capsule similar to those of related mucosal pathogens.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 8 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 16 Apr 1997
ACCESSION NUMBER: 1997:246716 CAPLUS
DOCUMENT NUMBER: 126:329201
TITLE: Highly conserved Neisseria meningitidis surface protein confers protection against experimental infection
AUTHOR(S): Martin, Denis; Cadieux, Nathalie; Hamel, Josee; Brodeur, Bernard R.
CORPORATE SOURCE: Unite de Recherche en Vaccinologie, Centre de Recherche en Infectiologie, Centre Hospitalier Universitaire de Quebec, Ste-Foy, QC, G1V 4G2, Can.
SOURCE: Journal of Experimental Medicine (1997), 185(7), 1173-1183
CODEN: JEMEAV; ISSN: 0022-1007
PUBLISHER: Rockefeller University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A new surface **protein**, named NspA, which is distinct from the previously described **Neisseria meningitidis** outer membrane **proteins** was **identified**. An NspA-specific mAb, named Me-1, reacted with 99% of the **meningococcal** strains tested indicating that the epitope recognized by this particular mAb is widely distributed and highly conserved. Western immunoblotting expts. indicated that mAb Me-1 is directed against a **protein** band with an approx. mol. mass of 22,000, but also recognized a minor **protein** band with an approx. mol. mass of 18,000. This mAb exhibited bactericidal activity against four **meningococcal** strains, two isolates of serogroup B, and one isolate from each serogroup A and C, and passively protected mice against an exptl. infection. To further characterize the NspA **protein** and to evaluate the protective potential of recombinant NspA **protein**, the nspA gene was **identified** and cloned into a low copy expression vector. **Nucleotide** sequencing of the **meningococcal** insert revealed an **ORF** of 525 **nucleotides** coding for a **polypeptide** of 174 **amino** acid residues, with a predicted mol. weight of 18,404 and a isoelec. point of 9.93. Three injections of either 10 or 20 μg of the affinity-purified recombinant NspA **protein** efficiently protected 80% of the mice against a **meningococcal** deadly challenge comparatively to the 20% observed in the control groups. The fact that the NspA **protein** can elicit the production of bactericidal and protective antibodies emphasize its potential as a vaccine candidate.
REFERENCE COUNT: 67 THERE ARE 67 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 9 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 24 Feb 1997
ACCESSION NUMBER: 1997:126125 CAPLUS
DOCUMENT NUMBER: 126:182080
TITLE: Molecular characterization of hpuAB, the hemoglobin-haptoglobin-utilization operon of Neisseria meningitidis
AUTHOR(S): Lewis, Lisa A.; Gray, Elizabeth; Wang, Ying-Ping; Roe, Bruce A.; Dyer, David W.
CORPORATE SOURCE: Department of Microbiology and Immunology, State

University of New York at Buffalo, Buffalo, NY, 14214, USA
SOURCE: Molecular Microbiology (1997), 23(4), 737-749
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We previously **identified** HpuB, an 85 kDa Fe-repressible **protein** required for utilization of Fe from, and binding to, Hb and the Hb-haptoglobin complex. The gene for hpuB was cloned from **Neisseria meningitidis** strain DNM2 and the predicted **amino** acid sequence indicates that HpuB is an outer membrane receptor belonging to the TonB family of high-affinity transport **proteins**. A second **open reading frame**, predicted to encode a 34.8 kDa lipoprotein, was discovered 5' to hpuB, and was designated hpuA. HpuA was **identified** in a total-membrane-**protein** preparation by construction of a mutant lacking HpuA. Acylation of HpuA was confirmed by [3H]-palmitic acid labeling of **meningococci**. Consensus promoter sequences were not apparent 5' to hpuB. The hpuA insertion mutation exerted a polar effect, abolishing expression of hpuB, suggesting that hpuA and hpuB are co-transcribed. The 3.5 kb polycistronic hpuAB mRNA was **identified** and shown to be transcriptionally repressed by iron. The transcriptional start site was **identified** 33 **nucleotides** 5' to the hpuA translational start site, appropriately positioned around consensus promoter and ferric uptake regulator (Fur)-box sequences. The structure of this operon suggests that HpuA-HpuB is a two-component receptor analogous to the bipartite transferrin receptor TbpB-TbpA.

L4 ANSWER 10 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 07 Feb 1997
ACCESSION NUMBER: 1997:88915 CAPLUS
DOCUMENT NUMBER: 126:127638
TITLE: Neisseria meningitidis tonB, exbB, and exbD genes: Ton-dependent utilization of protein-bound iron in neisseriae
AUTHOR(S): Stojiljkovic, Igor; Srinivasan, Nithya
CORPORATE SOURCE: Dep. Microbiol. and Immunology, Emory Univ., Atlanta, GA, 30322, USA
SOURCE: Journal of Bacteriology (1997), 179(3), 805-812
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have recently cloned and characterized the Hb receptor gene, hmbR, from **Neisseria meningitidis**. To **identify** addnl. **proteins** that are involved in Hb utilization, the **N. meningitidis** Hb utilization system was reconstituted in Escherichia coli. Five cosmids from **N. meningitidis** DNA library enabled a heme-requiring (hemA), HmbR-expressing mutant of E. coli to use Hb as both porphyrin and iron source. **Nucleotide** sequence anal. of DNA fragments subcloned from the Hb-complementing cosmids **identified** four **open reading frames**, three of them homologous to Pseudomonas putida, E. coli, and Haemophilus influenzae exbB, exbD, and tonB genes. The **N. meningitidis** TonB **proteins** is 28.8 to 33.6% identical to other Gram-neg. TonB **proteins**, while the **N. meningitidis**

ExbD **protein** shares between 23.3 and 34.3% identical **amino** acids with other ExbD and TolR **proteins**. The **N. meningitidis** ExbB **protein** was 24.7 to 36.1% homologous with other Gram-neg. ExbB and TolQ **proteins**. Complementation studies indicated that the neisserial Ton system cannot interact with the E. coli FhuA TonB-dependent outer membrane receptor. The **N. meningitidis** tonB mutant was unable to use Hb, Hb-haptoglobin complexes, transferrin, and lactoferrin as iron sources. Insertion of an antibiotic cassette in the 3' end of the exbD gene produced a leaky phenotype. Efficient usage of heme by **N. meningitidis** tonB and exbD mutants suggests the existence of a Ton-independent heme utilization mechanism. E. coli complementation studies and the anal. of **N. meningitidis** hmbR and hpu mutants suggested the existence of another Hb utilization mechanism in this organism.

REFERENCE COUNT: 70 THERE ARE 70 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 11 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Mar 1996
ACCESSION NUMBER: 1996:140979 CAPLUS
DOCUMENT NUMBER: 124:222276
TITLE: Inner core biosynthesis of lipooligosaccharide (LOS) in Neisseria meningitidis serogroup B: identification and role in LOS assembly of the α1,2 N-acetylglucosamine transferase (RfaK)
AUTHOR(S): Kahler, Charlene M.; Carlson, Russell W.; Rahman, M. Mahbubur; Martin, Larry E.; Stephens, David S.
CORPORATE SOURCE: Dep. Med., Emory Univ. Sch. Med. and Dep. Veterans Affairs Med. Cent., Atlanta, GA, USA
SOURCE: Journal of Bacteriology (1996), 178(5), 1265-73
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A lipooligosaccharide (LOS) mutant of **Neisseria meningitidis** serogroup B strain **NMB** (immunotype L3,7,9) was **identified** in a Tn916 (tetM) mutant bank by loss of reactivity with monoclonal antibody 3F11, which recognizes the terminal Galβ1→4GlcNAc epitope in the lacto-N-neotetraose moiety of the wild-type LOS structure. The mutant, designated 559, was found to express a truncated LOS of 3.0 kDa. Southern and PCR analyses demonstrated that there was a single intact Tn916 insertion (class I) in the mutant 559 chromosome. Linkage of the LOS phenotype and the Tn916 insertion (class I) in the mutant 559 chromosome. Linkage of the LOS phenotype and the Tn916 insertion was confirmed by transformation of the wild-type parent. **Nucleotide** sequence anal. of the region surrounding the transposition site revealed a 1,065-bp **open reading frame** (**ORF**). A homol. search of the GenBank/EMBL database revealed that the **amino** acid sequence of this **ORF** had 46.8% similarity and 21.2% identity with the α1,2 N-acetylglucosamine transferase (RfaK) from Salmonella typhimurium. Glycosyl composition and linkage anal. of the LOS produced by mutant 559 revealed that the lacto-N-neotetraose group which is attached to heptose I (HepI) and the N-acetylglucosamine and glucose residues that are attached to HepII in the inner core of the parental LOS were absent. These analyses also showed that the HepII residue in both the parent and the

mutant LOS were absent. These analyses also showed that the HepII residue in both the parent and the mutant LOS were absent. These analyses also showed that the HepII residue in both the parent and the mutant LOS mols. was phosphorylated, presumably by a phosphoethanolamine substituent. The insertion of nonpolar mols. was phosphorylated, presumably by a phosphoethanolamine substituent. The insertion of nonpolar and polar antibiotic resistance cartridges into the parental rfaK gene resulted in the expression of LOS with the same mobility as that produced by mutant 559. This result indicated that the inability to add the lacto-N-neotetraose group to the 559 LOS is not due to a polar effect on a gene(s) downstream of rfaK. Our data indicate that we have **identified** the **meningococcal** α1,2 N-acetylglucosamine transferase responsible for the addition of N-acetylglucosamine to HepII. We propose that the lack of α-chain extension from HepI in the LOS of mutant 559 may be due to structural constraints imposed by the incomplete biosynthesis of the LOS inner core.

L4 ANSWER 12 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 19 Dec 1995
ACCESSION NUMBER: 1995:988988 CAPLUS
DOCUMENT NUMBER: 124:78149
TITLE: Co-transcription of a homolog of the formamidopyrimidine- DNA glycosylase (fpg) and lysophosphatidic acid acyltransferase (nlaA) in Neisseria meningitidis
AUTHOR(S): Swartley, John S.; Stephens, David S.
CORPORATE SOURCE: Departments of Medicine and Microbiology and Immunology, Emory University School of Medicine, and Department of Veterans Affairs Medical Center, Atlanta, Georgia, USA
SOURCE: FEMS Microbiology Letters (1995), 134(2-3), 171-6
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors report the **identification** of an **open reading frame** in a serogroup B isolate of **Neisseria meningitidis** that exhibits high **nucleotide** and predicted **amino** acid identity with the fpg gene of Escherichia coli, and its product, formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase), a DNA repair enzyme. The authors further show that the **meningococcal** fpg is co-transcribed with nlaA, encoding a lysophosphatidic acid acyltransferase, and suggest that the DNA repair enzyme may be involved in the regulation of nlaA or its gene product.

L4 ANSWER 13 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 22 Jun 1995
ACCESSION NUMBER: 1995:630637 CAPLUS
DOCUMENT NUMBER: 123:221089
TITLE: Identification and characterization of pilG, a highly conserved pilus-assembly gene in pathogenic Neisseria
AUTHOR(S): Tonjum, Tone; Freitag, Nancy E.; Namork, Ellen; Koomey, Michael
CORPORATE SOURCE: Kaptein W. Wilhelmsen og Frues Bakteriologiske Institutt, Rikshospitalet (National Hospital), University of Oslo, Oslo, N-0027, Norway

SOURCE: Molecular Microbiology (1995), 16(3), 451-64
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Expression of type IV pili appears to be a requisite **determinant** of infectivity for the strict human pathogens Neisseria gonorrhoeae and **Neisseria meningitidis**. The assembly of these colonization factors is a complex process. This report describes a new pilus-assembly gene, pilG, that immediately precedes the gonococcal (Gc) pilD gene encoding the pre-pilin leader peptidase. The **nucleotide** sequence of this region revealed a single complete **open reading frame** whose derived **polypeptide** displayed significant identities to the pilus-assembly **protein** PilC of Pseudomonas aeruginosa and other polytopic integral cytoplasmic membrane constituents involved in **protein** export and competence. A unique **polypeptide** of Mr 38 kDa corresponding to the gene product was **identified**. A highly related gene and flanking sequences were cloned from a group B polysaccharide-producing strain of **N. meningitidis** (Mc). The results indicate that the pilG genes and genetic organization at these loci in Gc and Mc are extremely conserved. Hybridization studies strongly suggest that pilG-related genes exist in commensal Neisseria species and other species known to express type IV pili. Defined genetic lesions were created by using insertional and transposon mutagenesis and moved into the Gc and Mc chromosomes by allelic replacement. Chromosomal pilG insertion mutants were devoid of pili and displayed dramatically reduced competence for transformation. These findings could not be ascribed to pilin-gene alterations or to polarity exerted on pilD expression. The results indicated that PilG exerts its own independent role in Neisseria pilus biogenesis.

L4 ANSWER 14 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 26 Nov 1994
ACCESSION NUMBER: 1994:647460 CAPLUS
DOCUMENT NUMBER: 121:247460
TITLE: Identification and characterization of the Treponema pallidum tpn50 gene and OmpA homolog
AUTHOR(S): Hardham, John M.; Stamm, Lola V.
CORPORATE SOURCE: Sch. Med., Univ. North Carolina, Chapel Hill, NC, 27599, USA
SOURCE: Infection and Immunity (1994), 62(3), 1015-25
CODEN: INFIBR; ISSN: 0019-9567
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Treponema pallidum is a pathogenic spirochete that has no known genetic exchange mechanisms. In order to **identify** treponemal genes encoding surface and secreted **proteins**, we carried out TnphoA mutagenesis of a T. pallidum genomic DNA library in Escherichia coli. Several of the resulting clones expressed enzymically active T. pallidum-alkaline phosphatase fusion **proteins**. The DNA sequence of the 5' portion of a number of the treponemal genes was obtained and analyzed. A recombinant clone harboring plasmid p4A2 that encoded a treponemal **protein** with an approx. mol. mass of 50,000 Da was **identified**. Plasmid p4A2 contained an **open reading frame** of 1,251 **nucleotides** that resulted in a predicted **protein** of 417 **amino** acids with a calculated

mol. mass of 47,582 Da. We have named this gene tnp50 in accordance with the current nomenclature for T. pallidum genes. A 1.9-kb HincII-ClaI fragment from p4A2 that contained the tpn50 gene was subcloned to produce p4A2HC2. Comparison of the predicted **amino** acid sequence of TpN50 with **protein** sequences in the National Center for Biotechnol. Information data base indicated statistically significant homol. to the Pseudomonas sp. OprF, E. coli OmpA, Bordetella avium OmpA, **Neisseria meningitidis** RmpM, Neisseria gonorrhoeae PIII, Haemophilus influenzae P6, E. coli PAL and Legionella pneumophila PAL **proteins**. These **proteins** are all members of a family of outer membrane **proteins** that are present in Gram-neg. bacteria. The tnp50 gene complemented E. coli ompA mutations on the basis of two sep. criteria. First, morphometry and electron microscopy data showed that E. coli C386 (ompA lpp) cells harboring plasmid vector pEBH21 were rounded while cells of the same strain harboring p4A2HC2 (TpN50+), pWW2200 (OprF+), or pRD87 (OmpA+) were rod shaped. Second, E. coli BRE51 (MC4100 ΔsulA-ompA) cells harboring pEBH21 grew poorly at 42°C in minimal medium, while the growth of BRE51 cells harboring p4A2HC2 was similar to that of the parental MC4100 cells. These results demonstrate that the TpN50 **protein** is functionally equivalent to the E. coli OmpA **protein**. If TpN50 functions in a similar fashion in T. pallidum, then it may be localized to the treponemal outer membrane.

L4 ANSWER 15 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Jul 1994
ACCESSION NUMBER: 1994:406790 CAPLUS
DOCUMENT NUMBER: 121:6790
TITLE: Identification of six open reading frames in the Salmonella enterica subsp. enterica ser. Typhi viaB locus involved in Vi antigen production
AUTHOR(S): Waxin, H.; Virlogeux, I.; Kolyva, S.; Popoff, M. Y.
CORPORATE SOURCE: Unite Enterobac., Inst. Pasteur, Paris, 75724, Fr.
SOURCE: Research in Microbiology (1993), 144(5), 363-71
CODEN: RMCREW; ISSN: 0923-2508
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The Vi antigen of Salmonella enterica subsp. enterica ser. Typhi (hereafter referred to as Typhi) is a capsular polysaccharide consisting of a homopolymer of α-1,4 2-deoxy-2N-acetyl galacturonic acid (Felix and Pitt, 1934). **Determinants** of Vi antigen occupy two widely separated chromosomal loci, designated viaA and viaB. The viaB locus, specific to Vi expressing strains, maps at 92 min on the chromosome of Typhi (Johnson et al., 1965). Cloning and mol. anal. of this chromosomal region were reported previously (Hashimoto et al., 1991; Kolyva et al., 1992). Here the authors report on the **nucleotide** sequence of a 9.3-kb fragment located within the Typhi strain Ty2viaB locus. The dideoxy chain-termination method, using modified T7 DNA polymerase ("Sequenase"; USB Corp.) and universal forward and synthetic primers, was employed after subcloning of appropriate restriction fragments into M13 derivs. (Messing and Vieira, 1982). All the ends of restriction fragments used overlapped one another. DNA sequencing was performed at least twice on both strands. **Nucleotide** sequence data were analyzed using the Lipman-Pearson program (Lipman and Pearson, 1985). The sequence data have been submitted to the EMBL data library and were assigned accession number X67785. Examination of the

DNA sequence revealed six **open reading frames** (**ORF**), termed: tviA (Typhi Vi), tviB, tviC, tviD, tviE and tviF. All were transcribed in the same orientation. Their description is reported. Significant homol. was **detected** between TviB **protein** and AlgD (Deretic et al., 1987), a GDP-mannose dehydrogenase of Pseudomonas aeruginosa (26 % identity and 71 % similarity in 288 **amino** acids overlap) and between TviC **protein** and StrE (Pissowotzki et al., 1991), a TDP-glucose dehydratase of Streptomyces griseus (28 % identity and 68 % similarity in 326 **amino** acids overlap). A lipoprotein signal sequence (Hussain et al., 1982) with a potential cleavage site for signal peptidase II was found in the TviF sequence. TviF **protein** shared significant homol. to BexD (Kroll et al., 1990) and CtrA (Frosch et al., 1991) **proteins** (27 % identity and 72 % similarity in 280 **amino** acids overlap) which are involved in capsule export by Haemophilus influenzae and **Neisseria meningitidis**, resp. Studies designed to **determine** whether TviB and TviC **proteins** are involved in the biosynthesis, and TviF in the biogenesis, of the Vi antigen are presently under was in the authors' laboratory

L4 ANSWER 16 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 19 Mar 1994
ACCESSION NUMBER: 1994:126440 CAPLUS
DOCUMENT NUMBER: 120:126440
TITLE: Cloning, sequencing, expression, and complementation analysis of the Escherichia coli K1 kps region 1 gene, kpsE, and identification of an upstream open reading frame encoding a protein with homology to GutQ
AUTHOR(S): Cieslewicz, Michael J.; Steenbergen, Susan M.; Vimr, Eric R.
CORPORATE SOURCE: Dep. Vet. Pathobiol., Univ. Illinois, Urbana, IL, 61801, USA
SOURCE: Journal of Bacteriology (1993), 175(24), 8018-23
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The kps locus for polysialic acid capsule expression in Escherichia coli K1 is composed of a central group of biosynthetic neu genes, designated region 2, flanked on either side by region 1 or region 3 kps genes with poorly defined functions. Chromosomal mutagenesis with MudJ and subsequent complementation anal., maxicell and in vitro **protein** expression studies, and **nucleotide** sequencing **identified** the region 1 gene, kpsE, which encodes a 39-kDa **polypeptide**. Polarity of the kpsE::lacZ mutation suggests an operonic structure for region 1. KpsE is homologous to putative polysaccharide-translocation components previously **identified** in Haemophilus influenzae type b and **Neisseria meningitidis** group B. An **open reading frame** upstream of kpsE encodes a 35-kDa **polypeptide** with homol. to GutQ, a putative ATP-binding **protein** of unknown function encoded by gutQ of the glucitol-utilization operon. Whether expression of the gutQ homolog as the potential first gene of region 1 is required for polysialic acid synthesis or localization is presently unknown.

L4 ANSWER 17 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 16 Oct 1993

ACCESSION NUMBER: 1993:555703 CAPLUS
DOCUMENT NUMBER: 119:155703
TITLE: Phospholipid substitution of capsular polysaccharides and mechanisms of capsule formation in Neisseria meningitidis
AUTHOR(S): Frosch, Matthias; Mueller, Astrid
CORPORATE SOURCE: Inst. Med. Mikrobiol., Med. Hochsch. Hannover, Hannover, 3000/61, Germany
SOURCE: Molecular Microbiology (1993), 8(3), 483-93
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Within the capsule gene complex (cps) of **Neisseria meningitidis** two functional regions B and C are involved in surface translocation of the cytoplasmically synthesized capsular polysaccharide, which is a homopolymer of α-2,8-polyneuraminic acid. The region-C gene products share characteristics with transporter **proteins** of the ABC (ATP-binding cassette) superfamily of active transporters. For anal. of the role of region B in surface translocation of the capsular polysaccharide the authors purified the polysaccharides of region B- and region C-defective Escherichia coli clones by affinity chromatog. The mol. wts. of the polysaccharides were **determined** by gel filtration and the polysaccharides were analyzed for phospholipid substitution by polyacrylamide gel electrophoresis and immunoblotting. The results indicate that the full-size capsular polysaccharide with a phospholipid anchor is synthesized intracellularly and that lipid modification is a strong requirement for translocation of the polysaccharide to the cell surface. **Proteins** encoded by region B are involved in phospholipid substitution of the capsular polysaccharide. **Nucleotide** sequence anal. of region B revealed two **open reading frames**, which encode **proteins** with mol. masses of 45.1 and 48.7 kDa.

L4 ANSWER 18 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 24 Jul 1993
ACCESSION NUMBER: 1993:423575 CAPLUS
DOCUMENT NUMBER: 119:23575
TITLE: Sequence and functional analysis of the cloned Neisseria meningitidis CMP-NeuNAc synthetase
AUTHOR(S): Edwards, Ulrike; Frosch, Matthias
CORPORATE SOURCE: Inst. Med. Mikrobiol., Med. Hochsch. Hannover, Hannover, 3000/61, Germany
SOURCE: FEMS Microbiology Letters (1992), 96(2-3), 161-6
CODEN: FMLED7; ISSN: 0378-1097
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The CMP-N-acetylneuraminic acid (CMP-NeuNAc) synthetase gene of **N. meningitidis** group B is located on a 2.3-kb EcoRI fragment within the cps gene cluster. **Nucleotide** sequence **determination** of the gene encoding the CMP-NeuNAc synthetase revealed a 515-bp **open reading frame** that can encode a 18.9-kDa **protein**. A computer data base scan revealed a 59.4% identity to the CMP-NeuNAc synthetase gene of Escherichia coli K1. Enzymic activity was confirmed in vitro and in vivo. Transformation of the CMP-NeuNAc defective E. coli K1 strain EV5 with the **meningococcal** CMP-NeuNAc synthetase could complement the defect in E. coli.

L4 ANSWER 19 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 29 May 1993
ACCESSION NUMBER: 1993:210900 CAPLUS
DOCUMENT NUMBER: 118:210900
TITLE: Cloning and expression in Escherichia coli of opc, the gene for an unusual class 5 outer membrane protein from Neisseria meningitidis (meningococci/surface antigen)
AUTHOR(S): Olyhoek, A. J. M.; Sarkari, J.; Bopp, M.; Morelli, G.; Achtman, M.
CORPORATE SOURCE: Max-Planck Inst. Mol. Genet., Berlin, 1000, Germany
SOURCE: Microbial Pathogenesis (1991), 11(4), 249-57
CODEN: MIPAEV; ISSN: 0882-4010
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A genomic library was constructed in a λgt11 vector using chromosomal DNA from a **meningococcal** serogroup A strain and plaques expressing the class 5C **protein** were recognized by **screening** with specific monoclonal antibodies. The opc insert was subcloned into a multicopy plasmid which induced expression of that **protein** in Escherichia coli as a surface-exposed major outer membrane **protein**. The **nucleotide** sequence of opc is typical of an outer membrane **protein** with a promoter and terminator region, a leader **peptide** which is cleaved during expression and a complete **open reading frame**. Unlike other **meningococcal** class 5 **proteins** or gonococcal P.II **proteins**, the sequence did not contain any pentanucleotide repeats and the sequence showed little homol. to these other functionally related **proteins**. However, the predicted **amino** acid sequence of the mature **protein** for opc showed 27% similarity to that for a second opa gene cloned from the same **meningococcal** strain. This is the first report of cloning and expression of a functional **meningococcal** gene encoding a class 5 outer membrane **protein** in E. coli.

L4 ANSWER 20 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 10 Jan 1993
ACCESSION NUMBER: 1993:1812 CAPLUS
DOCUMENT NUMBER: 118:1812
TITLE: Molecular mechanisms of capsule expression in Neisseria meningitidis
AUTHOR(S): Frosch, M.; Bousset, Kristine
CORPORATE SOURCE: Inst. Med. Mikrobiol., Med. Hochsch. Hannover, Hannover, 3000/61, Germany
SOURCE: Neisseriae 1990, Proc. Int. Pathog. Neisseria Conf., 7th (1991), Meeting Date 1990, 517-21. Editor(s): Achtman, Mark. de Gruyter: Berlin, Germany.
CODEN: 58FNAF
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Within the cps gene complex encoding the capsular polysaccharide of **N. meningitidis** 5 functional regions could be assigned: enzymes for biosynthesis of capsular polysaccharide are encoded by region A; region B directs translocation of the polysaccharide from the cytoplasm to the periplasm and region C provides the genetic information for polysaccharide transport from

periplasm to the cell surface; regions D and E presumably play a regulatory role in the capsular polysaccharide biosynthesis. To understand the mol. mechanisms of capsular polysaccharide transport, the gene products of region C were analyzed and their functional role in the translocation process was investigated. The complete **nucleotide** sequence of the 4.3-kb EcoRI fragment of region C was **determined** This fragment has been shown to encompass the limits of region C. Four **open reading frames** were **detected** that could encode for a 42-kDa, 41-kDa, 26-kDa, and 25-kDa **proteins**. The genes encoding these **proteins** have been termed ctrA, ctrB, ctrC, and ctrD, resp., according to the 4 **open reading frames**. CtrA could be assigned to the outer membrane whereas **proteins** CtrB and CtrC were found associated with the inner membrane. Secondary structure prediction for CtrA revealed 8 membrane-spanning beta-strands with a potential to form a pore. The formation of a pore for specific translocation of capsular polysaccharide is supported by the fact that mutants with an isolated defect in the ctrA locus retain the capsular polysaccharide in the periplasm and are not able to translocate it to the cell surface. An 80% of CtrD to BexA of Haemophilus influenzae type B was found. This **protein** is encoded within the bridge region of the H. influenzae capsule gene locus and because of homologies to Escherichia coli MalK at the ATP-binding site, it is thought to function as energizer for the translocation of capsular polysaccharide to the cell surface.

L4 ANSWER 21 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 16 May 1992
ACCESSION NUMBER: 1992:188853 CAPLUS
DOCUMENT NUMBER: 116:188853
TITLE: CDNA and derived amino acid sequence of rabbit nasal cytochrome P450NMb (P450IIG1), a unique isozyme possibly involved in olfaction
AUTHOR(S): Ding, Xinxin; Porter, Todd D.; Peng, Hwei Ming; Coon, Minor J.
CORPORATE SOURCE: Med. Sch., Univ. Michigan, Ann Arbor, MI, 48109-0606, USA
SOURCE: Archives of Biochemistry and Biophysics (1991), 285(1), 120-5
CODEN: ABBIA4; ISSN: 0003-9861
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Olfactory-specific cytochrome P450NMb was previously purified to electrophoretic homogeneity from microsomes of rabbit nasal mucosa in this laboratory In the present study, a cDNA library made from poly(A)+ RNA from rabbit nasal mucosa was **screened** with antibodies to this P450, and 8 immunopos. clones were isolated and characterized. The sequence **determined** from 2 overlapping clones contained an **open reading frame** of 1446 **nucleotides**, with the predicted first 39 **amino** acids corresponding to residues 12 to 50 of purified **NMb**, except for position 46, where Leu was encoded instead of the Glu residue that was found earlier by Edman degradation anal. The complete **polypeptide**, including residues 1 to 11, contains 494 **amino** acid residues and has a mol. weight of 56,640. Sequence comparisons indicated that **NMb** is more than 50% identical to members of the rabbit P450 gene II family, including IIB4, IIC3, IIC5, IIE1, and IIE2, and 83% identical to rat P450olf1 (IIG1).

Hybridization of **NMb** to electrophoretically fractionated rabbit nasal poly(A)+ RNA revealed 3.6- and 2.1-kb species, but with a probe derived from the 3'-nontranslated portion of the cDNA only the 3.6-kb band was observed, suggesting the use of alternate polyadenylation sites or splicing. In agreement with the known tissue-specific distribution of **NMb protein, NMb** transcripts were found in olfactory mucosa, but not in liver, lung, intestine, or kidney. Genomic hybridization anal. indicated that there may be only one copy of the **NMb** gene present in the rabbit genome.

L4 ANSWER 22 OF 22 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Apr 1990
ACCESSION NUMBER: 1990:133318 CAPLUS
DOCUMENT NUMBER: 112:133318
TITLE: The class 1 outer membrane protein of Neisseria meningitidis: gene sequence and structural and immunological similarities to gonococcal porins
AUTHOR(S): Barlow, A. K.; Heckels, J. E.; Clarke, I. N.
CORPORATE SOURCE: Med. Sch., Univ. Southampton, Southampton, SO9 4XY, UK
SOURCE: Molecular Microbiology (1989), 3(2), 131-9
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The class 1 **protein** is a major **protein** of the outer membrane of **N. meningitidis**, and an important immunodeterminant in humans. The complete **nucleotide** sequence for the structural gene of a class 1 **protein** has been **determined** The sequence predicts a **protein** of 374 **amino** acids, preceded by a typical signal **peptide** of 19 residues. The hydropathy profile of the predicted **protein** sequence resembles that of the Escherichia coli and gonococcal porins. The predicted **protein** sequence of the class 1 **protein** exhibits considerable structural similarity to the gonococcal porins PIA and PIB. Western blot studies also reveal immunol. conserved domains between the class 1 **protein**, PIA and PIB. A restriction fragment from the class 1 gene hybridizes to gonococcal genomic fragments in Southern blots. In addition to the class 1 gene coding region there is a large **open reading frame** on the opposite strand.

FILE 'MEDLINE' ENTERED AT 14:37:28 ON 15 AUG 2005

FILE 'BIOSIS' ENTERED AT 14:37:28 ON 15 AUG 2005

FILE 'EMBASE' ENTERED AT 14:37:28 ON 15 AUG 2005

FILE 'WPIDS' ENTERED AT 14:37:28 ON 15 AUG 2005

FILE 'CONFSCI' ENTERED AT 14:37:28 ON 15 AUG 2005

FILE 'SCISEARCH' ENTERED AT 14:37:28 ON 15 AUG 2005

FILE 'JICST-EPLUS' ENTERED AT 14:37:28 ON 15 AUG 2005

FILE 'JAPIO' ENTERED AT 14:37:28 ON 15 AUG 2005

L5 81 S L4
L6 26 DUP REM L5 (55 DUPLICATES REMOVED)

L6 ANSWER 1 OF 26 WPIDS
ACCESSION NUMBER: 2005-464877 [47] WPIDS
CROSS REFERENCE: 1999-327407 [27]
DOC. NO. CPI: C2005-141464
TITLE: New Neisserial nucleic acids useful for diagnosing and/or treating bacterial infections, in particular meningitis and septicemia caused by Neisseria meningitidis and Neisseria gonorrhea.
DERWENT CLASS: B04 D16
INVENTOR(S): GRANDI, G; MASIGNANI, V; PIZZA, M; RAPPUOLI, R; SCARLATO, V
PATENT ASSIGNEE(S): (CHIR) CHIRON SRL
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 6914131	B1	20050705	(200547)*		613

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 6914131	B1 CIP of	WO 1998-IB1665	19981009
		US 1999-303518	19990430

PRIORITY APPLN. INFO: US 1999-303518 19990430; WO 1998-IB1665 19981009
AN 2005-464877 [47] WPIDS
CR 1999-327407 [27]
AB US 6914131 B UPAB: 20050725
NOVELTY - An isolated nucleic acid molecule having an **open reading frame** that comprises:
(a) any of 7 fully defined **nucleotide** sequences of 894-1887 bp (SEQ **ID** NO: 125, 127, 131, 463, 465, 569 or 571);
(b) a fragment of (a) at least 25 **nucleotides** in length;
(c) a **nucleotide** sequence completely complementary at the same length to (a) or (b); or
(d) a **nucleotide** sequence having 90% or greater sequence identity to (a), (b) or (c).
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) an isolated nucleic acid molecule which can hybridize to a nucleic acid molecule as cited above under high stringency conditions;
(2) a recombinant vector comprising an isolated nucleic acid molecule as cited above, and control elements that are operably linked to the nucleic acid molecule, where a coding sequence within the

nucleic acid molecule can be transcribed and translated in a host cell, and at least one of the control elements is heterologous to the coding sequence;

(3) a host cell transformed with the recombinant vector of (2); and

(4) a method of producing a recombinant **polypeptide**, comprising providing a population of host cells of (3), and culturing the population of cells under conditions where the **polypeptide** encoded by the coding sequence present in the recombinant vector is expressed.

ACTIVITY - Antibacterial; Immunosuppressive; Antiinflammatory. No biological data given.

MECHANISM OF ACTION - Vaccine.

USE - The methods and compositions of the present invention are useful for diagnosing and/or treating Neisserial bacterial infections, in particular meningitis and septicemia caused by **Neisseria meningitidis** and Neisseria gonorrhea.

Dwg.0/20

L6 ANSWER 2 OF 26 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2003-248057 [24] WPIDS
CROSS REFERENCE: 2003-300862 [29]
DOC. NO. CPI: C2003-063917
TITLE: New Neisserial adhesin A protein and nucleic acids, useful for preventing or treating meningitis, particularly bacterial meningitis, and bacteremia, and for eliciting an systemic and/or mucosal immunity.
DERWENT CLASS: B04 D16
INVENTOR(S): ARICO, M; COMANDUCCI, M; ARICO, M B
PATENT ASSIGNEE(S): (CHIR) CHIRON SPA; (CHIR) CHIRON SRL; (CHIR-N) CHIRON SPA
COUNTRY COUNT: 101
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003010194	A2	20030206	(200324)*	EN	40
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW					
EP 1412381	A2	20040428	(200429)	EN	
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI SK TR					
AU 2002355197	A1	20030217	(200452)		
BR 2002011494	A	20040817	(200457)		
JP 2005503785	W	20050210	(200511)		142
CN 1582297	A	20050216	(200535)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003010194	A2	WO 2002-IB3396	20020726
EP 1412381	A2	EP 2002-790218	20020726

		WO 2002-IB3396	20020726
AU 2002355197	A1	AU 2002-355197	20020726
BR 2002011494	A	BR 2002-11494	20020726
		WO 2002-IB3396	20020726
JP 2005503785	W	WO 2002-IB3396	20020726
		JP 2003-515553	20020726
CN 1582297	A	CN 2002-822187	20020906

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1412381	A2 Based on	WO 2003010194
AU 2002355197	A1 Based on	WO 2003010194
BR 2002011494	A Based on	WO 2003010194
JP 2005503785	W Based on	WO 2003010194

PRIORITY APPLN. INFO: GB 2002-11025 20020514; GB 2001-18401 20010727; GB 2001-21591 20010906

AN 2003-248057 [24] WPIDS

CR 2003-300862 [29]

AB WO2003010194 A UPAB: 20050603

NOVELTY - A protein (I) comprising a 362, 398, 405, 364, 400, 407, 391, 393, 405, 107, 355, 357, 323, or 319 residue amino acid sequence (designated P1), given in the specification, an amino acid sequence having at least 50 % identity to (P1), or a fragment of (P1), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) a nucleic acid encoding (I);

(2) an immunogenic composition comprising a Neisserial adhesin A (NadA) protein and/or nucleic acid encoding a NadA protein;

(3) raising an antibody response or for protecting against Neisserial infection in a mammal by administering the immunogenic composition;

(4) purifying processed adhesion and penetration protein (App) by expressing a gene encoding App protein in a non-Neisserial host cell, and purifying processed App protein from the culture medium;

(5) purified protein obtainable by the process of (4);

(6) preventing the attachment of a Neisserial cell to an epithelial cell, where the ability of one or more App, ORF40 and/or NadA to bind to the epithelial cell is blocked, or where protein expression is inhibited;

(7) nucleic acid comprising a fragment of x or more nucleotides from nucleic acid which encodes App, ORF40 or NadA, where x is at least 8;

(8) a Neisseria bacterium in which App, ORF40 and/or NadA has been knocked out;

(9) preventing the attachment of a Neisserial cell to an epithelial cell, where App, ORF40 and/or NadA has a mutation which inhibits its activity;

(10) a mutant protein comprising a sequence of App, ORF40 and/or NadA or its fragment, where one or more amino acids of the amino acid sequence is/are mutated;

(11) nucleic acid encoding the mutant protein of (10);

(12) producing the nucleic add of (11) by providing source nucleic acid encoding App, ORF40 or NadA, and performing mutagenesis on the source nucleic acid to provide nucleic acid encoding a mutant protein;

(13) screening for compounds which inhibit the binding of a

Neisserial cell to an epithelial cell;

(14) a compound identified using the method of (13);

(15) a composition comprising an E. coli bacterium which expresses App and/or ORF40 (and optionally, NadA and Po) an epithelial cell;

(16) preparing an outer membrane vesicle (OMV) from a non-Neisserial host cell that expresses a gene encoding App, ORF40 or NadA protein;

(17) an OMV obtained from the methods of (16), or from a non-Neisserial host cell that expresses a gene encoding App, ORF40 or NadA protein;

(18) a protein comprising the amino acid sequence of App, except that:

(a) amino acid Asp-158, His-115 and/or Ser-267 is mutated;

(b) one or more amino acids between Ser-1064 and Arg-1171 is mutated; or

(c) one or more amino acids Phe-956, Asn-957, Ala-1178 and Asn-1179 is mutated;

(19) a protein comprising the amino acid sequence of App except that amino acid Asp-158, His-115 and/or Ser-267 is mutated, or one or more amino acid between Ser1064-Arg1171 is mutated;

(20) a protein comprising the amino acid sequence of a processed App where:

(a) the processed App does not comprise the C-terminus domain downstream of an autoproteolytic cleavage site in full length App; or

(b) the C-terminus of the processed App is Phe-956 or Ala-1178;

(21) a protein comprising a 956, 1178, 914, 1136, 222, 278 or 501 residue amino acid sequence, given in the specification, a sequence at least 50 % identical to any of these sequences, or a fragment of these sequences; and

(22) a nucleic acid encoding the protein of (21).

ACTIVITY - Antibacterial; Immunostimulant.

No biological data is given.

MECHANISM OF ACTION - Vaccine.

USE - The NadA protein, or nucleic acid encoding NadA protein is useful in the manufacture of a medicament for preventing Neisserial infection in a mammal, such as an infection of Neisseria meningitidis from hypervirulent lineages ET-5, EY-37 and cluster A4 (claimed). The NadA protein is useful for preventing or treating diseases, specifically meningitis (particularly bacterial meningitis) and bacteremia, and for eliciting an systemic and/or mucosal immunity.

Dwg.0/40

L6 ANSWER 3 OF 26 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 2001208178 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11254622
TITLE: Mu-like Prophage in serogroup B Neisseria meningitidis coding for surface-exposed antigens.
AUTHOR: Masignani V; Giuliani M M; Tettelin H; Comanducci M; Rappuoli R; Scarlato V
CORPORATE SOURCE: Department of Molecular Biology, IRIS, Chiron S.p.A., 53100 Siena, Italy.
SOURCE: Infection and immunity, (2001 Apr) 69 (4) 2580-8. Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200104

Searcher : Shears 571-272-2528

ENTRY DATE: Entered STN: 20010417
Last Updated on STN: 20010417
Entered Medline: 20010412

AB Sequence analysis of the genome of Neisseria meningititdis serogroup B revealed the presence of an approximately 35-kb region inserted within a putative gene coding for an ABC-type transporter. The region contains 46 **open reading frames**, 29 of which are colinear and homologous to the genes of Escherichia coli Mu phage. Two prophages with similar organizations were also found in serogroup A **meningococcus**, and one was found in Haemophilus influenzae. Early and late phage functions are well preserved in this family of Mu-like prophages. Several regions of atypical **nucleotide** content were **identified**. These likely represent genes acquired by horizontal transfer. Three of the acquired genes are shown to code for surface-associated antigens, and the encoded **proteins** are able to induce bactericidal antibodies.

L6 ANSWER 4 OF 26 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2001285397 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11179344
TITLE: exl, an exchangeable genetic island in Neisseria meningitidis.
AUTHOR: Kahler C M; Blum E; Miller Y K; Ryan D; Popovic T; Stephens D S
CORPORATE SOURCE: Department of Medicine and Department of Microbiology and Immunology, Emory University School of Medicine, Atlanta, Georgia, USA.. charlene.kahler@monash.edu.au
CONTRACT NUMBER: AI-33517 (NIAID)
SOURCE: Infection and immunity, (2001 Mar) 69 (3) 1687-96. Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF319527; GENBANK-AF319528; GENBANK-AF319529; GENBANK-AF319530; GENBANK-AF319531; GENBANK-AF319532; GENBANK-AF319533; GENBANK-AF319534; GENBANK-AF319535; GENBANK-AF319536; GENBANK-AF319537
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20030403
Entered Medline: 20010524

AB The genetic structure and evolution of a novel exchangeable **meningococcal** genomic island was defined for the important human pathogen **Neisseria meningitidis**. In 125 **meningococcal** strains tested, one of three unrelated **nucleotide** sequences, designated exl (exchangeable locus), was found between a gene required for heme utilization, hemO, and col, encoding a putative Escherichia coli collagenase homologue. The 5' boundary of each exl cassette was the stop codon of hemO, whereas the 3' boundary was delineated by a 33-bp repeat containing neisserial uptake sequences located downstream of col. One of the three alternative exl cassettes contained the **meningococcal** hemoglobin receptor gene, hmbR (exl3). In other **meningococcal** strains, hmbR was absent from the genome and was replaced by either a **nucleotide** sequence containing a novel **open reading frame**, exl2, or a cassette containing exl3. The **proteins** encoded by exl2 and exl3 had no significant

amino acid homology to HmbR but contained six motifs that are also present in the lipoprotein components of the lactoferrin (LbpB), transferrin (TbpB), and hemoglobin-haptoglobin (HpuA) uptake systems. To **determine** the evolutionary relationships among **meningococci** carrying hmbR, exl2, or exl3, isolates representing 92 electrophoretic types were examined. hmbR was found throughout the population structure of **N. meningitidis** (genetic distance, >0.425), whereas exl2 and exl3 were found in clonal groups at genetic distances of <0.2. The commensal neisserial species were **identified** as reservoirs for all of the exl cassettes found in **meningococci**. The structure of these cassettes and their correlation with clonal groups emphasize the extensive gene pool and frequent horizontal DNA transfer events that contribute to the evolution and virulence of **N. meningitidis**.

L6 ANSWER 5 OF 26 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

ACCESSION NUMBER: 2002:201462 BIOSIS
DOCUMENT NUMBER: PREV200200201462
TITLE: Sequence analysis of the plasmid pF3031 of the Brazilian purpuric fever clone of Haemophilus influenzae biogroup aegyptius.
AUTHOR(S): Mukhopadhyay, S. [Reprint author]; Actis, L. A. [Reprint author]
CORPORATE SOURCE: Miami University, Oxford, OH, USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 302. print.
Meeting Info.: 101st General Meeting of the American Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for Microbiology.
ISSN: 1060-2011.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 20 Mar 2002
Last Updated on STN: 20 Mar 2002

AB Haemophilus influenzae biogroup aegyptius (Haemophilus aegyptius) is the causative agent of Brazilian purpuric fever (BPF), a pediatric infection that causes disseminated purpura and vascular collapse. Initial plasmid analysis showed that Brazilian BPF and nonBPF isolates contain a 24-MDa cryptic plasmid. Attempts to cure this plasmid, in order to **determine** its virulence role, using different approaches failed. Therefore, we decided to subclone different regions of pF3031, which is present in the prototype strain F3031, and **determine** their **nucleotide** sequence. Computer analysis of a 13-kb EcoRI fragment showed the presence of 13 **open reading frames** (**ORFs**), all transcribed in the same direction. BLASTx analysis showed that 10 of them have homology with the virB, tra, lvh, and cag genes that encode components of type IV bacterial secretion systems in bacteria like Agrobacterium tumefaciens, Bartonella henselae, Rickettsia prowazekii, Brucella abortus, B. suis, Escherichia coli, Legionella pneumophila, and Helicobacter pylori. This region is flanked by an **ORF** transcribed in the opposite direction that has homology to a hypothetical gene found in Actinobacillus actinomycetemcomitans and Yersinia enterocolitica. A 7.5-kb BglII fragment contains six putative **ORFs**, five of which appear to be part of a single

polycistronic operon that is flanked by a HP1 tail fiber homolog. Two of these genes have no homologs in the database, while the other four are related to Xylella fastidiosa and **Neisseria meningitidis** hypothetical genes. In addition, pF3031 contains **ORFs** related to the A. rhizogenes virC1 gene and genes encoding a X. fastidiosa conjugal transfer **protein**, an A. actinomycetemcomitans ATPase, and the VirD4 **protein** of R. prowazekii and A. tumefaciens. Southern blotting showed that the noninvasive strain F1947 carries a 24-MDa plasmid related to pF3031, although the two plasmids showed some differences in their restriction patterns. These results show that pF3031 carries genetic **determinants** that were not found in the genome of other H. influenzae strains studied previously, some of which are important virulence **determinants**.

L6 ANSWER 6 OF 26 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-647603 [62] WPIDS
CROSS REFERENCE: 2000-062150 [05]; 2000-318079 [27]; 2001-557776 [62]; 2001-582163 [65]
DOC. NO. CPI: C2000-195957
TITLE: Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections.
DERWENT CLASS: B04 D16
INVENTOR(S): FRAZER, C; GALEOTTI, C; GRANDI, G; HICKEY, E; MASIGNANI, V; MORA, M; PETERSON, J; PIZZA, M; RAPPUOLI, R; RATTI, G; SCARLATO, V; SCARSELLI, M; TETTELIN, H; VENTER, J C; FRAZER, C M
PATENT ASSIGNEE(S): (CHIR) CHIRON CORP; (GENO-N) INST GENOMIC RES; (CHIR-N) CHIRON SPA
COUNTRY COUNT: 92
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000066791	A1	20001109	(200062)*	EN	669
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000032492	A	20001117	(200111)		
EP 1185691	A1	20020313	(200225)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
CN 1359426	A	20020717	(200268)		
BR 2000010361	A	20030610	(200341)		
JP 2003527079	W	20030916	(200362)		723
NZ 515654	A	20031219	(200404)		
RU 2233328	C2	20040727	(200456)		
MX 2001011047	A1	20031201	(200470)		
AU 2005200246	A1	20050217	(200517)#		
AU 780308	B2	20050317	(200523)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000066791	A1	WO 2000-US5928	20000308

AU 2000032492	A	AU 2000-32492	20000308
EP 1185691	A1	EP 2000-910392	20000308
		WO 2000-US5928	20000308
CN 1359426	A	CN 2000-809820	20000308
BR 2000010361	A	BR 2000-10361	20000308
		WO 2000-US5928	20000308
JP 2003527079	W	JP 2000-615413	20000308
		WO 2000-US5928	20000308
NZ 515654	A	NZ 2000-515654	20000308
		WO 2000-US5928	20000308
RU 2233328	C2	WO 2000-US5928	20000308
		RU 2001-132325	20000308
MX 2001011047	A1	WO 2000-US5928	20000308
		MX 2001-11047	20011030
AU 2005200246	A1 Div ex	AU 2000-32492	20000308
		AU 2005-200246	20050121
AU 780308	B2	AU 2000-32492	20000308

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000032492	A Based on	WO 2000066791
EP 1185691	A1 Based on	WO 2000066791
BR 2000010361	A Based on	WO 2000066791
JP 2003527079	W Based on	WO 2000066791
NZ 515654	A Div in	NZ 528063
	Based on	WO 2000066791
RU 2233328	C2 Based on	WO 2000066791
MX 2001011047	A1 Based on	WO 2000066791
AU 780308	B2 Previous Publ.	AU 2000032492
	Based on	WO 2000066791

PRIORITY APPLN. INFO: GB 2000-4695 20000228; US 1999-132068P 19990430; WO 1999-US23573 19991008; AU 2005-200246 20050121

AN 2000-647603 [62] WPIDS

CR 2000-062150 [05]; 2000-318079 [27]; 2001-557776 [62]; 2001-582163 [65]

AB WO 200066791 A UPAB: 20050411

NOVELTY - A nucleic acid (I) comprising the full length genome of **Neisseria meningitidis** B (**NMB**) (II) or one or more **NMB open reading frames**, all given in the specification, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method for **identifying** an **amino** acid (aa) sequence comprising searching for putative **open reading frames** or **protein coding sequences** within (I);

(2) a method for producing a **protein** comprising expressing a **protein** comprising an aa sequence **identified** by the above method;

(3) a method for **identifying** a **protein** in **N. meningitidis** comprising producing a **protein** as in (2), producing an antibody which binds to the **protein** and **determining** whether the antibody recognizes a **protein** produced by **N. meningitidis**;

(4) nucleic acid comprising an **open reading frame** or **protein coding sequence identified** by the method of (1);

(5) a **protein** (V) obtained by the method of (2);

(6) a nucleic acid (II) comprising a fragment of (I);

(7) a nucleic acid (III) comprising a **nucleotide** sequence with greater than 50% sequence identity to (I);

(8) a nucleic acid complementary to (I), (II) or (III);

(9) a **protein** (VI) comprising an aa sequence encoded within (I);

(10) a **protein** (VII) comprising an aa sequence having greater then 50% sequence identity to an aa sequence encoded within (I);

(11) a **protein** (VIII) comprising a fragment of an aa sequence encoded within (I);

(12) nucleic acid (IV) encoding one of (VI)-(VIII);

(13) a computer, a computer memory, a computer storage medium or a computer database containing (I), (II) or (III);

(14) a polyclonal or monoclonal antibody which binds to (VI)-(VIII) or (V);

(15) a nucleic acid probe comprising nucleic acid (I), (II), (III) or (IV); and

(16) an amplification primer comprising nucleic acid (I), (II), (III) or (IV).

ACTIVITY - Antibacterial.

No biological data is given.

MECHANISM OF ACTION - Vaccine; Gene therapy.

USE - Nucleic acids (I), (II), (III) or (IV), **protein** (VI)-(VIII) or (V) and/or antibody which binds to (VI)-(VIII) or (V) can be used in a composition for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for **detecting** the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria (claimed).

The computer, computer memory, computer storage medium or computer database can be used in a search to **identify open reading frames** (**ORFs**) or coding sequences within (I).

ADVANTAGE - The DNA sequences provide further opportunities to find antigenic or immunogenic **proteins** which are more effective in vaccines than the outer membrane **proteins** currently used.

Dwg.0/18

L6 ANSWER 7 OF 26 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2000-318079 [27] WPIDS

CROSS REFERENCE: 2000-062150 [05]; 2000-647603 [62]; 2001-557776 [62]; 2001-582163 [65]

DOC. NO. NON-CPI: N2000-238677

DOC. NO. CPI: C2000-096408

TITLE: Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): FRAZER, C M; GALEOTTI, C; HICKEY, E; MASIGNANI, V; MORA, M; PETERSON, J; PIZZA, M; RAPPUOLI, R; RATTI, G; SCARLATO, V; SCARSELLI, M; TETTELIN, H; VENTER, C J; VENTER, J C; GIULIO, A; GRANDI, G; FRASER, C M

PATENT ASSIGNEE(S): (CHIR) CHIRON CORP; (GENO-N) INST GENOMIC RES

COUNTRY COUNT: 91
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000022430	A2	20000420	(200027)*	EN	
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000012022	A	20000501	(200036)		
EP 1144998	A2	20011017	(200169)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
CN 1338005	A	20020227	(200234)		
BR 9914374	A	20020917	(200264)		
RU 2223492	C2	20040210	(200424)		
JP 2004511201	W	20040415	(200426)		
NZ 511540	A	20040528	(200437)		
AU 2004201096	A1	20040408	(200456)#		
MX 2001003557	A1	20040401	(200478)		
EP 1559795	A2	20050803	(200551)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000022430	A2	WO 1999-US23573	19991008
AU 2000012022	A	AU 2000-12022	19991008
EP 1144998	A2	EP 1999-970470	19991008
		WO 1999-US23573	19991008
CN 1338005	A	CN 1999-814108	19991008
BR 9914374	A	BR 1999-14374	19991008
		WO 1999-US23573	19991008
RU 2223492	C2	WO 1999-US23573	19991008
		RU 2001-112411	19991008
JP 2004511201	W	WO 1999-US23573	19991008
		JP 2000-576277	19991008
NZ 511540	A	NZ 1999-511540	19991008
		WO 1999-US23573	19991008
AU 2004201096	A1 Div ex	AU 2000-12022	19991008
		AU 2004-201096	20040311
MX 2001003557	A1	WO 1999-US23573	19991008
		MX 2001-3557	20010406
EP 1559795	A2 Div ex	EP 1999-970470	19991008
		EP 2005-75407	19991008

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000012022	A Based on	WO 2000022430
EP 1144998	A2 Based on	WO 2000022430
BR 9914374	A Based on	WO 2000022430
RU 2223492	C2 Based on	WO 2000022430
JP 2004511201	W Based on	WO 2000022430

Searcher : Shears 571-272-2528

NZ 511540	A	Div in Based on	NZ 528121 WO 2000022430
MX 2001003557	A1	Based on	WO 2000022430
EP 1559795	A2	Div ex	EP 1144998

PRIORITY APPLN. INFO: US 1999-132068P 19990430; US 1998-103794P 19981009; AU 2004-201096 20040311

AN 2000-318079 [27] WPIDS

CR 2000-062150 [05]; 2000-647603 [62]; 2001-557776 [62]; 2001-582163 [65]

AB WO 200022430 A UPAB: 20050810

NOVELTY - Nucleic acids from **Neisseria meningitidis** comprising any of the following nucleic acid (NA) sequences: 1-961 and 1068, or even-numbered sequences, 962-1044, given in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) **Identifying** an **amino** acid sequence, comprising searching for putative **open reading frames** or **protein coding sequences** within on or more specified **Neisseria meningitidis nucleotide** sequences;

(2) producing a **protein**, comprising the step of expressing a **protein** comprising an **amino** acid sequence **identified** using the above method;

(3) **identifying** a **protein** in **N. meningitidis**, comprising the steps of producing a **protein** using the method of (2), producing an antibody which binds to the **protein**, and **determining** whether the antibody recognizes a **protein** produced by **N. meningitidis**;

(4) nucleic acid comprising an **open reading frame** or **protein-coding sequence identified** using the above method;

(5) a **protein** obtained by the method of (2);

(6) nucleic acid comprising a **nucleotide** sequence having greater than 50% sequence identity to any of the nucleic acid (NA) sequences: 1-961 and 1068, or even-numbered sequences, 962-1044;

(7) nucleic acid comprising a fragment of any **nucleotide** sequence from 1-961 and 1068 or even numbered sequences, 962 to 1044;

(8) nucleic acid complementary to the nucleic acid of (6)-(7);

(9) a **protein** comprising an **amino** acid sequence encoded within one or more of the **N. meningitidis nucleotide** sequences as above;

(10) a **protein** comprising an **amino** acid sequence having greater than 50% sequence identity to an **amino** acid sequence encoded within one or more of the **N. meningitidis nucleotide** sequences above;

(11) a **protein** comprising a fragment of an **amino** acid sequence selected from the group consisting of one or more odd-numbered sequences, 963-1037, **amino** acid sequences having greater than 50% identity with one or more odd numbered sequences, 963-1045, **amino** acid sequences encoded within one or more of the **N. meningitidis nucleotide** sequences above;

(12) nucleic acid encoding a **protein** as above;

(13) a computer, a computer memory, a computer storage medium or a computer database containing the **nucleotide** sequence of a nucleic acid of (6)-(7);

(14) a computer, a computer memory, a computer storage medium or a computer database containing one or more of the **N. meningitidis nucleotide** sequences;1-961;

(15) a polyclonal or monoclonal antibody which binds to the **protein** of ((5), or (9)-(11);

(16) a nucleic acid probe comprising nucleic acid according to (3), (5)-(8) or (12);

(17) an amplification primer comprising nucleic acid according to (3), (5)-(8) or (12);

(18) a composition comprising:

(a) nucleic acid according to (4), (6)-(7) or (12);

(b) **protein** according to (9)-(11); and/or

(c) an antibody according to (15);

(19) use of the composition of (18) as a medicament or as a diagnostic reagent;

(20) use of the composition of (18) in the manufacture of:

(a) a medicament for treating or preventing infection due to Neisserial bacteria, and/or

(b) a diagnostic reagent for **detecting** the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria; and

(21) treating a patient, comprising administering to the patient a therapeutically effective amount of the composition of (18).

ACTIVITY - Anti-bacterial. No biological data is given.

MECHANISM OF ACTION - Vaccine. No biological data is given.

USE - The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria (all claimed). For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes.

ADVANTAGE - Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.

Dwg.0/18

L6 ANSWER 8 OF 26 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER: 1999270944 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10338491

TITLE: Antigenic and molecular conservation of the gonococcal NspA protein.

AUTHOR: Plante M; Cadieux N; Rioux C R; Hamel J; Brodeur B R; Martin D

CORPORATE SOURCE: Unite de Recherche en Vaccinologie, Centre Hospitalier Universitaire de Quebec et Universite Laval, Ste-Foy, Quebec, Canada G1V 4G2.

SOURCE: Infection and immunity, (1999 Jun) 67 (6) 2855-61. Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

Searcher : Shears 571-272-2528

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U52066; GENBANK-U52069
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990714
Last Updated on STN: 19990714
Entered Medline: 19990628

AB A low-molecular-weight **protein** named NspA (neisserial surface **protein** A) was recently **identified** in the outer membrane of all **Neisseria meningitidis** strains tested. Antibodies directed against this **protein** were shown to protect mice against an experimental **meningococcal** infection. Hybridization experiments clearly demonstrated that the nspA gene was also present in the genomes of the 15 Neisseria gonorrhoeae strains tested. Cloning and sequencing of the nspA gene of N. gonorrhoeae B2 revealed an **open reading frame** of 525 **nucleotides** coding for a **polypeptide** of 174 **amino** acid residues, with a calculated molecular weight of 18,316 and a pI of 10.21. Comparison of the predicted **amino** acid sequence of the NspA **polypeptides** from the gonococcal strains B2 and FA1090, together with that of the **meningococcal** strain 608B, revealed an identity of 93%, suggesting that the NspA **protein** is highly conserved among pathogenic Neisseria strains. The level of identity rose to 98% when only the two gonococcal predicted NspA **polypeptides** were compared. To evaluate the level of antigenic conservation of the gonococcal NspA **protein**, monoclonal antibodies (MAbs) were generated. Four of the seven NspA-specific MAbs described in this report recognized their corresponding epitope in 100% of the 51 N. gonorrhoeae strains tested. Radioimmunobinding assays clearly indicated that the gonococcal NspA **protein** is exposed at the surface of intact cells.

L6 ANSWER 9 OF 26 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 1998175678 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9515923
TITLE: Characterization of the gene cassette required for biosynthesis of the (alpha1-->6)-linked N-acetyl-D-mannosamine-1-phosphate capsule of serogroup A Neisseria meningitidis.
AUTHOR: Swartley J S; Liu L J; Miller Y K; Martin L E; Edupuganti S; Stephens D S
CORPORATE SOURCE: Department of Medicine, Emory University School of Medicine, and Department of Veterans Affairs Medical Center, Atlanta 30303, Georgia, USA.
CONTRACT NUMBER: R01 AI40247-01 (NIAID)
SOURCE: Journal of bacteriology, (1998 Mar) 180 (6) 1533-9.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF019760
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980422
Last Updated on STN: 20030321
Entered Medline: 19980414

AB The (alpha1-->6)-linked N-acetyl-D-mannosamine-1-phosphate **meningococcal** capsule of serogroup A **Neisseria**

meningitidis is biochemically distinct from the sialic acid-containing capsules produced by other disease-associated **meningococcal** serogroups (e.g., B, C, Y, and W-135). We defined the genetic cassette responsible for expression of the serogroup A capsule. The cassette comprised a 4,701-bp **nucleotide** sequence located between the outer membrane capsule transporter gene, ctrA, and galE, encoding the UDP-glucose-4-epimerase. Four **open reading frames** (**ORFs**) not found in the genomes of the other **meningococcal** serogroups were **identified**. The first serogroup A **ORF** was separated from ctrA by a 218-bp intergenic region. Reverse transcriptase (RT) PCR and primer extension studies of serogroup A mRNA showed that all four **ORFs** were cotranscribed in the opposite orientation to ctrA and that transcription of the **ORFs** was initiated from the intergenic region by a sigma-70-type promoter that overlapped the ctrA promoter. The first **ORF** exhibited 58% **amino** acid identity with the UDP-N-acetyl-D-glucosamine (UDP-GlcNAc) 2-epimerase of Escherichia coli, which is responsible for the conversion of UDP-GlcNAc into UDP-N-acetyl-D-mannosamine. Polar or nonpolar mutagenesis of each of the **ORFs** resulted in an abrogation of serogroup A capsule production as **determined** by colony immunoblots and enzyme-linked immunosorbent assay. Replacement of the serogroup A biosynthetic gene cassette with a serogroup B cassette by transformation resulted in capsule switching from a serogroup A capsule to a serogroup B capsule. These data indicate that assembly of the serogroup A capsule likely begins with monomeric UDP-GlcNAc and requires **proteins** encoded by three other genes found in the serogroup A **N. meningitidis**-specific operon located between ctrA and galE.

L6 ANSWER 10 OF 26 MEDLINE on STN DUPLICATE 5

ACCESSION NUMBER: 1998149315 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9489671
TITLE: Molecular characterization of LbpB, the second lactoferrin-binding protein of Neisseria meningitidis.
AUTHOR: Pettersson A; Prinz T; Umar A; van der Biezen J; Tommassen J
CORPORATE SOURCE: Department of Molecular Cell Biology and Institute of Biomembranes, Utrecht University, The Netherlands.. A.M.Pettersson-Fernholm@biol.ruu.nl
SOURCE: Molecular microbiology, (1998 Feb) 27 (3) 599-610. Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF022781
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980430
Last Updated on STN: 19980430
Entered Medline: 19980420

AB The lbpA gene of **Neisseria meningitidis** encodes an outer membrane lactoferrin-binding **protein** and shows homology to the transferrin-binding **protein**, TbpA. Previously, we have **detected** part of an **open reading frame** upstream of lbpA. The putative product of this **open reading frame**, tentatively designated lbpB, showed homology to the

transferrin-binding **protein** TbpB, suggesting that the lactoferrrin receptor, like the transferrin receptor, consists of two **proteins**. The complete **nucleotide** sequence of lbpB was **determined**. The gene encodes a 77.5 kDa **protein**, probably a lipoprotein, with homology, 33% identity to the TbpB of **N. meningitidis**. A unique feature of LbpB is the presence of two stretches of negatively charged residues, which might be involved in lactoferrin binding. Antisera were raised against synthetic **peptides** corresponding to the C-terminal part of the putative **protein** and used to demonstrate that the gene is indeed expressed. Consistent with the presence of a putative Fur binding site upstream of the lbpB gene, expression of both LbpA and LbpB was proved to be iron regulated in Western blot experiments. The LbpB **protein** appeared to be less stable than TbpB in SDS-containing sample buffer. Isogenic mutants lacking either LbpA or LbpB exhibited a reduced ability to bind lactoferrin. In contrast to the lbpB mutant, the lbpA mutant was completely unable to use lactoferrin as a sole source of iron.

L6 ANSWER 11 OF 26 MEDLINE on STN DUPLICATE 6
ACCESSION NUMBER: 1998367129 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9701807
TITLE: Structure and function of repetitive sequence elements associated with a highly polymorphic domain of the Neisseria meningitidis PilQ protein.
AUTHOR: Tonjum T; Caugant D A; Dunham S A; Koomey M
CORPORATE SOURCE: Institute of Microbiology, National Hospital, Oslo, Norway.. tone.tonjum@rh.uio.no
CONTRACT NUMBER: AI27837 (NIAID)
SOURCE: Molecular microbiology, (1998 Jul) 29 (1) 111-24. Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF066056
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981118

AB Secretins are a large family of **proteins** associated with membrane translocation of macromolecular complexes, and a subset of this family, termed PilQ **proteins**, is required for type IV pilus biogenesis. We analysed the status of PlIQ expression in **Neisseria meningitidis** (Mc) and found that PlIQ mutants were non-piliated and deficient in the expression of pilus-associated phenotypes. Sequence analysis of the 5' portion of the pilQ **ORF** of the serogroup B Mc strain 44/76 showed the presence of seven copies of a repetitive sequence element, in contrast to the situation in N. gonorrhoeae (Gc) strains, which carry either two or three copies of the repeat. The derived **amino** acid sequence of the consensus **nucleotide** repeat was an octapeptide PAKQQAAA, designated as the small basic repeat (SBR). This gene segment was studied in more detail in a collection of 52 Mc strains of diverse origin by **screening** for variability in the size of the PCR-generated DNA fragments spanning the SBRs. These strains were found to harbour from four to seven copies of the repetitive element. No association between the number of copies and the serogroup, geographic origin or multilocus genotype of the strains

was evident. The presence of polymorphic repeat elements in Mc PilQ is unprecedented within the secretin family. To address the potential function of the repeat containing domain, Mc strains were constructed so as to express chimeric PilQ molecules in which the number of SBR repeats was increased or in which the repeat containing domain was replaced in toto by the corresponding region of the Pseudomonas aeruginosa (Pa) PilQ **protein**. Although the strain expressing PilQ with an increased number of SBRs was identical to the parent strain in pilus phenotypes, a strain expressing PilQ with the equivalent Pa domain had an eightfold reduction in pilus expression level. The findings suggest that the repeat containing domain of PilQ influences Mc pilus expression quantitatively but not qualitatively.

L6 ANSWER 12 OF 26 MEDLINE on STN DUPLICATE 7
ACCESSION NUMBER: 97313195 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9169799
TITLE: Identification and characterization of a DNA region involved in the export of capsular polysaccharide by Actinobacillus pleuropneumoniae serotype 5a.
AUTHOR: Ward C K; Inzana T J
CORPORATE SOURCE: Center for Molecular Medicine and Infectious Diseases, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Polytechnic Institute and State University, Blacksburg 24061-0342, USA.
SOURCE: Infection and immunity, (1997 Jun) 65 (6) 2491-6. Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U36397
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970630
Last Updated on STN: 19990129
Entered Medline: 19970619

AB Actinobacillus pleuropneumoniae synthesizes a serotype-specific capsular polysaccharide that acts as a protective barrier to phagocytosis and complement-mediated killing. To begin understanding the role of A. pleuropneumoniae capsule in virulence, we sought to **identify** the genes involved in capsular polysaccharide export and biosynthesis. A 5.3-kb XbaI fragment of A. pleuropneumoniae serotype 5a J45 genomic DNA that hybridized with DNA probes specific for the Haemophilus influenzae type b cap export region was cloned and sequenced. This A. pleuropneumoniae DNA fragment encoded four **open reading frames**, designated cpxDCBA. The **nucleotide** and predicted **amino** acid sequences of cpxDCBA contained a high degree of homology to the capsule export genes of H. influenzae type b bexDCBA, **Neisseria meningitidis** group B ctrABCD, and, to a lesser extent, Escherichia coli K1 and K5 kpsE and kpsMT. When present in trans, the cpxDCBA gene cluster complemented kpsM::TnphoA or kpsT::TnphoA mutations, **determined** by enzyme immunoassay and by restored sensitivity to a K5-specific bacteriophage. A cpxCB probe hybridized to genomic DNA from all A. pleuropneumoniae serotypes tested, indicating that this DNA was conserved among serotypes. These data suggest that A. pleuropneumoniae produces a group II family capsule similar to those of related mucosal pathogens.

L6 ANSWER 13 OF 26 MEDLINE on STN DUPLICATE 8

ACCESSION NUMBER: 97258610 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9104804
TITLE: Highly conserved Neisseria meningitidis surface protein confers protection against experimental infection.
AUTHOR: Martin D; Cadieux N; Hamel J; Brodeur B R
CORPORATE SOURCE: Unite de Recherche en Vaccinologie, Centre de Recherche en Infectiologie, Centre Hospitalier Universitaire de Quebec, Ste-Foy, Canada.
SOURCE: Journal of experimental medicine, (1997 Apr 7) 185 (7) 1173-83.
Journal code: 2985109R. ISSN: 0022-1007.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U52066
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970523
Last Updated on STN: 19970523
Entered Medline: 19970514

AB A new surface **protein**, named NspA, which is distinct from the previously described **Neisseria meningitidis** outer membrane **proteins** was **identified**. An NspA-specific mAb, named Me-1, reacted with 99% of the **meningococcal** strains tested indicating that the epitope recognized by this particular mAb is widely distributed and highly conserved. Western immunoblotting experiments indicated that mAb Me-1 is directed against a **protein** band with an approximate molecular mass of 22,000, but also recognized a minor **protein** band with an approximate molecular mass of 18,000. This mAb exhibited bactericidal activity against four **meningococcal** strains, two isolates of serogroup B, and one isolate from each serogroup A and C, and passively protected mice against an experimental infection. To further characterize the NspA **protein** and to evaluate the protective potential of recombinant NspA **protein**, the nspA gene was **identified** and cloned into a low copy expression vector. **Nucleotide** sequencing of the **meningococcal** insert revealed an **ORF** of 525 **nucleotides** coding for a **polypeptide** of 174 **amino** acid residues, with a predicted molecular weight of 18,404 and a isoelectric point of 9.93. Three injections of either 10 or 20 microg of the affinity-purified recombinant NspA **protein** efficiently protected 80% of the mice against a **meningococcal** deadly challenge comparatively to the 20% observed in the control groups. The fact that the NspA **protein** can elicit the production of bactericidal and protective antibodies emphasize its potential as a vaccine candidate.

L6 ANSWER 14 OF 26 MEDLINE on STN DUPLICATE 9
ACCESSION NUMBER: 97158676 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9006036
TITLE: Neisseria meningitidis tonB, exbB, and exbD genes: Ton-dependent utilization of protein-bound iron in Neisseriae.
AUTHOR: Stojiljkovic I; Srinivasan N
CORPORATE SOURCE: Department of Microbiology and Immunology, Emory University, Atlanta, Georgia 30322, USA.. stojiljk@microbio.emory.edu
SOURCE: Journal of bacteriology, (1997 Feb) 179 (3) 805-12.

Searcher : Shears 571-272-2528

Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U77738
ENTRY MONTH: 199702
ENTRY DATE: Entered STN: 19970313
Last Updated on STN: 19970313
Entered Medline: 19970228

AB We have recently cloned and characterized the hemoglobin (Hb) receptor gene, hmbR, from **Neisseria meningitidis**. To **identify** additional **proteins** that are involved in Hb utilization, the **N. meningitidis** Hb utilization system was reconstituted in Escherichia coli. Five cosmids from **N. meningitidis** DNA library enabled a heme-requiring (hemA), HmbR-expressing mutant of E. coli to use Hb as both porphyrin and iron source. **Nucleotide** sequence analysis of DNA fragments subcloned from the Hb-complementing cosmids **identified** four **open reading frames**, three of them homologous to Pseudomonas putida, E. coli, and Haemophilus influenzae exbB, exbD, and tonB genes. The **N. meningitidis** TonB **protein** is 28.8 to 33.6% identical to other gram-negative TonB **proteins**, while the **N. meningitidis** ExbD **protein** shares between 23.3 and 34.3% identical **amino** acids with other ExbD and TolR **proteins**. The **N. meningitidis** ExbB **protein** was 24.7 to 36.1% homologous with other gram-negative ExbB and TolQ **proteins**. Complementation studies indicated that the neisserial Ton system cannot interact with the E. coli FhuA TonB-dependent outer membrane receptor. The **N. meningitidis** tonB mutant was unable to use Hb, Hb-haptoglobin complexes, transferrin, and lactoferrin as iron sources. Insertion of an antibiotic cassette in the 3' end of the exbD gene produced a leaky phenotype. Efficient usage of heme by **N. meningitidis** tonB and exbD mutants suggests the existence of a Ton-independent heme utilization mechanism. E. coli complementation studies and the analysis of **N. meningitidis** hmbR and hpu mutants suggested the existence of another Hb utilization mechanism in this organism.

L6 ANSWER 15 OF 26 MEDLINE on STN DUPLICATE 10
ACCESSION NUMBER: 97206152 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9157245
TITLE: Molecular characterization of hpuAB, the haemoglobin-haptoglobin-utilization operon of Neisseria meningitidis.
AUTHOR: Lewis L A; Gray E; Wang Y P; Roe B A; Dyer D W
CORPORATE SOURCE: Department of Microbiology and Immunology, State University of New York at Buffalo 14214, USA.. llewis@rex.uokhsc.edu
CONTRACT NUMBER: AI23357 (NIAID)
SOURCE: Molecular microbiology, (1997 Feb) 23 (4) 737-49.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U18558; GENBANK-U73112; GENBANK-X69214;

GENBANK-X78939; GENBANK-X78941; GENBANK-Z15130
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970602
Last Updated on STN: 20021218
Entered Medline: 19970520

AB We previously **identified** HpuB, an 85 kDa Fe-repressible **protein** required for utilization of Fe from, and binding to, haemoglobin and the haemoglobin-haptoglobin complex. The gene for hpuB was cloned from **Neisseria meningitidis** strain DNM2 and the predicted **amino** acid sequence indicates that HpuB is an outer membrane receptor belonging to the TonB family of high-affinity transport **proteins**. A second **open reading frame**, predicted to encode a 34.8 kDa lipoprotein, was discovered 5' to hpuB, and was designated hpuA. HpuA was **identified** in a total-membrane-**protein** preparation by construction of a mutant lacking HpuA. Acylation of HpuA was confirmed by [3H]-palmitic acid labelling of **meningococci**. Consensus promoter sequences were not apparent 5' to hpuB. The hpuA insertion mutation exerted a polar effect, abolishing expression of hpuB, suggesting that hpuA and hpuB are co-transcribed. The 3.5 kb polycistronic hpuAB mRNA was **identified** and shown to be transcriptionally repressed by iron. The transcriptional start site was **identified** 33 **nucleotides** 5' to the hpuA translational start site, appropriately positioned around consensus promoter and ferric uptake regulator (Fur)-box sequences. The structure of this operon suggests that HpuA-HpuB is a two-component receptor analogous to the bipartite transferrin receptor TbpB-TbpA.

L6 ANSWER 16 OF 26 MEDLINE on STN DUPLICATE 11
ACCESSION NUMBER: 96200094 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8631701
TITLE: Inner core biosynthesis of lipooligosaccharide (LOS) in Neisseria meningitidis serogroup B: identification and role in LOS assembly of the alpha1,2 N-acetylglucosamine transferase (RfaK).
AUTHOR: Kahler C M; Carlson R W; Rahman M M; Martin L E; Stephens D S
CORPORATE SOURCE: Division of Infectious Diseases, Department of Medicine, Emory University School of Medicine, Atlanta, Georgia, USA.
CONTRACT NUMBER: 2-P41-RR05351-06 (NCRR)
SOURCE: Journal of bacteriology, (1996 Mar) 178 (5) 1265-73. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U58765
ENTRY MONTH: 199607
ENTRY DATE: Entered STN: 19960715
Last Updated on STN: 19980206
Entered Medline: 19960703

AB A lipooligosaccharide (LOS) mutant of **Neisseria meningitidis** serogroup B strain **NMB** (immunotype L3,7,9) was **identified** in a Tn916 (tetM) mutant bank by loss of reactivity with monoclonal antibody 3F11, which recognizes the terminal Galbeta1-->4GlcNAc epitope in the lacto-N-neotetraose moiety of the wild-type LOS structure. The mutant, designated 559, was found

to express a truncated LOS of 3.0 kDa. Southern and PCR analyses demonstrated that there was a single intact Tn916 insertion (class I) in the mutant 559 chromosome. Linkage of the LOS phenotype and the Tn916 insertion was confirmed by transformation of the wild-type parent. **Nucleotide** sequence analysis of the region surrounding the transposition site revealed a 1,065-bp **open reading frame** (**ORF**). A homology search of the GenBank/EMBL database revealed that the **amino** acid sequence of this **ORF** had 46.8% similarity and 21.2% identity with the alpha1,2 N-acetylglucosamine transferase (RfaK) from Salmonella typhimurium. Glycosyl composition and linkage analysis of the LOS produced by mutant 559 revealed that the lacto-N-neotetraose group which is attached to heptose I (HepI) and the N-acetylglucosamine and glucose residues that are attached to HepII in the inner core of the parental LOS were absent. These analyses also showed that the HepII residue in both the parent and the mutant LOS molecules was phosphorylated, presumably by a phosphoethanolamine substituent. The insertion of nonpolar and polar antibiotic resistance cartridges into the parental rfaK gene resulted in the expression of LOS with the same mobility as that produced by mutant 559. This result indicated that the inability to add the lacto-N-neotetraose group to the 559 LOS is not due to a polar effect on a gene(s) downstream of rfaK. Our data indicate that we have **identified** the **meningococcal** alpha1,2 N-acetylglucosamine transferase responsible for the addition of N-acetylglucosamine to HepII. We propose that the lack of alpha-chain extension from HepI in the LOS of mutant 559 may be due to structural constraints imposed by the incomplete biosynthesis of the LOS inner core.

L6 ANSWER 17 OF 26 MEDLINE on STN DUPLICATE 12
ACCESSION NUMBER: 96037790 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7565106
TITLE: Identification and characterization of pilG, a highly conserved pilus-assembly gene in pathogenic Neisseria.
AUTHOR: Tonjum T; Freitag N E; Namork E; Koomey M
CORPORATE SOURCE: Kaptein W. Wilhelmsen og Frues Bakteriologiske Institutt, Rikshospitalet (National Hospital), University of Oslo, Norway.
CONTRACT NUMBER: AI27837 (NIAID)
M01 RR 00042 (NCRR)
SOURCE: Molecular microbiology, (1995 May) 16 (3) 451-64.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U19579; GENBANK-U19580; GENBANK-U32588
ENTRY MONTH: 199511
ENTRY DATE: Entered STN: 19951227
Last Updated on STN: 19951227
Entered Medline: 19951108

AB Expression of type IV pili appears to be a requisite **determinant** of infectivity for the strict human pathogens Neisseria gonorrhoeae and **Neisseria meningitidis**. The assembly of these colonization factors is a complex process. This report describes a new pilus-assembly gene, pilG, that immediately precedes the gonococcal (Gc) pilD gene encoding the pre-pilin leader peptidase. The **nucleotide** sequence of this region revealed

a single complete **open reading frame** whose derived **polypeptide** displayed significant identities to the pilus-assembly **protein** PilC of Pseudomonas aeruginosa and other polytopic integral cytoplasmic membrane constituents involved in **protein** export and competence. A unique **polypeptide** of M(r) 38 kDa corresponding to the gene product was **identified**. A highly related gene and flanking sequences were cloned from a group B polysaccharide-producing strain of **N. meningitidis** (Mc). The results indicate that the pilG genes and genetic organization at these loci in Gc and Mc are extremely conserved. Hybridization studies strongly suggest that pilG-related genes exist in commensal Neisseria species and other species known to express type IV pili. Defined genetic lesions were created by using insertional and transposon mutagenesis and moved into the Gc and Mc chromosomes by allelic replacement. Chromosomal pilG insertion mutants were devoid of pili and displayed dramatically reduced competence for transformation. These findings could not be ascribed to pilin-gene alterations or to polarity exerted on pilD expression. The results indicated that PilG exerts its own independent role in neisserial pilus biogenesis.

L6 ANSWER 18 OF 26 MEDLINE on STN DUPLICATE 13
ACCESSION NUMBER: 96102858 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8586265
TITLE: Co-transcription of a homologue of the formamidopyrimidine-DNA glycosylase (fpg) and lysophosphatidic acid acyltransferase (nlaA) in Neisseria meningitidis.
AUTHOR: Swartley J S; Stephens D S
CORPORATE SOURCE: Department of Medicine, Emory University School of Medicine, Atlanta, Georgia 30303, USA.
CONTRACT NUMBER: AI-3351 (NIAID)
SOURCE: FEMS microbiology letters, (1995 Dec 15) 134 (2-3) 171-6.
Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U21808
ENTRY MONTH: 199603
ENTRY DATE: Entered STN: 19960404
Last Updated on STN: 20020815
Entered Medline: 19960322

AB We report the **identification** of an **open reading frame** in a serogroup B isolate of **Neisseria meningitidis** that exhibits high **nucleotide** and predicted **amino** acid identity with the fpg gene of Escherichia coli, and its product, formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase), a DNA repair enzyme. We further show that the **meningococcal** fpg is co-transcribed with nlaA, encoding a lysophosphatidic acid acyltransferase, and suggest that the DNA repair enzyme may be involved in the regulation of nlaA or its gene product.

L6 ANSWER 19 OF 26 MEDLINE on STN DUPLICATE 14
ACCESSION NUMBER: 94156449 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8112835
TITLE: Identification and characterization of the Treponema

pallidum tpn50 gene, an ompA homolog.
AUTHOR: Hardham J M; Stamm L V
CORPORATE SOURCE: Department of Microbiology and Immunology, School of Medicine, University of North Carolina, Chapel Hill 27599.
CONTRACT NUMBER: 1 UO1 AI31496 (NIAID)
3 T32 AI07001 (NIAID)
AI24976 (NIAID)
SOURCE: Infection and immunity, (1994 Mar) 62 (3) 1015-25.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U02628
ENTRY MONTH: 199403
ENTRY DATE: Entered STN: 19940406
Last Updated on STN: 19940406
Entered Medline: 19940330

AB Treponema pallidum is a pathogenic spirochete that has no known genetic exchange mechanisms. In order to **identify** treponemal genes encoding surface and secreted **proteins**, we carried out TnphoA mutagenesis of a T. pallidum genomic DNA library in Escherichia coli. Several of the resulting clones expressed enzymatically active T. pallidum-alkaline phosphatase fusion **proteins**. The DNA sequence of the 5' portion of a number of the treponemal genes was obtained and analyzed. A recombinant clone harboring plasmid p4A2 that encoded a treponemal **protein** with an approximate molecular mass of 50,000 Da was **identified**. Plasmid p4A2 contained an **open reading frame** of 1,251 **nucleotides** that resulted in a predicted **protein** of 417 **amino** acids with a calculated molecular mass of 47,582 Da. We have named this gene tpn50 in accordance with the current nomenclature for T. pallidum genes. A 1.9-kb HincII-ClaI fragment from p4A2 that contained the tpn50 gene was subcloned to produce p4A2HC2. Comparison of the predicted **amino** acid sequence of TpN50 with **protein** sequences in the National Center for Biotechnology Information data base indicated statistically significant homology to the Pseudomonas sp. OprF, E. coli OmpA, Bordetella avium OmpA, **Neisseria meningitidis** RmpM, Neisseria gonorrhoeae PIII, Haemophilus influenzae P6, E. coli PAL, and Legionella pneumophila PAL **proteins**. These **proteins** are all members of a family of outer membrane **proteins** that are present in gram-negative bacteria. The tpn50 gene complemented E. coli ompA mutations on the basis of two separate criteria. First, morphometry and electron microscopy data showed that E. coli C386 (ompA lpp) cells harboring plasmid vector pEBH21 were rounded while cells of the same strain harboring p4A2HC2 (TpN50+), pWW2200 (OprF+), or pRD87 (OmpA+) were rod shaped. Second, E. coli BRE51 (MC4100 delta sulA-ompA) cells harboring pEBH21 grew poorly at 42 degrees C in minimal medium, while the growth of BRE51 cells harboring p4A2HC2 was similar to that of the parental MC4100 cells. These results demonstrate that the TpN50 **protein** is functionally equivalent to the E. coli OmpA **protein**. If TpN50 functions in a similar fashion in T. pallidum, then it may be localized to the treponemal outer membrane.

L6 ANSWER 20 OF 26 MEDLINE on STN DUPLICATE 15
ACCESSION NUMBER: 94075243 MEDLINE

(2)

DOCUMENT NUMBER: PubMed ID: 8253690
TITLE: Cloning, sequencing, expression, and complementation analysis of the Escherichia coli K1 kps region 1 gene, kpsE, and identification of an upstream open reading frame encoding a protein with homology to GutQ.
AUTHOR: Cieslewicz M J; Steenbergen S M; Vimr E R
CORPORATE SOURCE: Department of Veterinary Pathobiology, University of Illinois at Urbana-Champaign 61801.
CONTRACT NUMBER: AI23039 (NIAID)
SOURCE: Journal of bacteriology, (1993 Dec) 175 (24) 8018-23. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L19929
ENTRY MONTH: 199401
ENTRY DATE: Entered STN: 19940203
Last Updated on STN: 19940203
Entered Medline: 19940110

AB The kps locus for polysialic acid capsule expression in Escherichia coli K1 is composed of a central group of biosynthetic neu genes, designated region 2, flanked on either side by region 1 or region 3 kps genes with poorly defined functions. Chromosomal mutagenesis with MudJ and subsequent complementation analysis, maxicell and in vitro **protein** expression studies, and **nucleotide** sequencing **identified** the region 1 gene, kpsE, which encodes a 39-kDa **polypeptide**. Polarity of the kpsE::lacZ mutation suggests an operonic structure for region 1. KpsE is homologous to putative polysaccharide-translocation components previously **identified** in Haemophilus influenzae type b and **Neisseria meningitidis** group B. An **open reading frame** upstream of kpsE encodes a 35-kDa **polypeptide** with homology to GutQ, a putative ATP-binding **protein** of unknown function encoded by gutQ of the glucitol utilization operon. Whether expression of the gutQ homolog as the potential first gene of region 1 is required for polysialic acid synthesis or localization is presently unknown.

L6 ANSWER 21 OF 26 MEDLINE on STN DUPLICATE 16
ACCESSION NUMBER: 93316845 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8326861
TITLE: Phospholipid substitution of capsular polysaccharides and mechanisms of capsule formation in Neisseria meningitidis.
AUTHOR: Frosch M; Muller A
CORPORATE SOURCE: Institut fur Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Germany.
SOURCE: Molecular microbiology, (1993 May) 8 (3) 483-93. Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Z13995
ENTRY MONTH: 199308
ENTRY DATE: Entered STN: 19930820
Last Updated on STN: 19970203
Entered Medline: 19930806

Searcher : Shears 571-272-2528

AB Within the capsule gene complex (cps) of **Neisseria meningitidis** two functional regions B and C are involved in surface translocation of the cytoplasmically synthesized capsular polysaccharide, which is a homopolymer of alpha-2,8 polyneuraminic acid. The region-C gene products share characteristics with transporter **proteins** of the ABC (ATP-binding cassette) superfamily of active transporters. For analysis of the role of region B in surface translocation of the capsular polysaccharide we purified the polysaccharides of region B- and region C-defective Escherichia coli clones by affinity chromatography. The molecular weights of the polysaccharides were **determined** by gel filtration and the polysaccharides were analysed for phospholipid substitution by polyacrylamide gel electrophoresis and immunoblotting. The results indicate that the full-size capsular polysaccharide with a phospholipid anchor is synthesized intracellularly and that lipid modification is a strong requirement for translocation of the polysaccharide to the cell surface. **Proteins** encoded by region B are involved in phospholipid substitution of the capsular polysaccharide. **Nucleotide** sequence analysis of region B revealed two **open reading frames**, which encode **proteins** with molecular masses of 45.1 and 48.7 kDa.

L6 ANSWER 22 OF 26 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 17

ACCESSION NUMBER: 1992:523115 BIOSIS
DOCUMENT NUMBER: PREV199294131190; BA94:131190
TITLE: SEQUENCE AND FUNCTIONAL ANALYSIS OF THE CLONED NEISSERIA-MENINGITIDIS CMP-NEUNAC SYNTHETASE.
AUTHOR(S): EDWARDS U [Reprint author]; FROSCH M
CORPORATE SOURCE: INSTITUT MEDIZINISCHE MIKROBIOLOGIE, MEDIZINISCHE HOCHSCHULE HANNOVER, 3000 HANNOVER 61, GER
SOURCE: FEMS Microbiology Letters, (1992) Vol. 96, No. 2-3, pp. 161-166.
CODEN: FMLED7. ISSN: 0378-1097.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 19 Nov 1992
Last Updated on STN: 24 Dec 1992

AB The CMP-N-acetylneuraminic acid (CMP-NeuNAc) synthetase gene of **Neisseria meningitidis** group B is located on a 2.3-kb EcoRI fragment within the cps gene cluster. **Nucleotide** sequence **determination** of the gene encoding the CMP-NeuNAc synthetase revealed a 515-bp **open reading frame** that can encode a 18.9-kDa **protein**. A computer data base scan revealed a 59.4% identity to the CMP-NeuNAc synthetase gene of E. coli K1. Enzymatic activity was confirmed in vitro and in vivo. Transformation of the CMP-NeuNAc defective E. coli K1 strain EV5 with the **meningococcal** CMP-NeuNAc synthetase could complement the defect in E. coli.

L6 ANSWER 23 OF 26 MEDLINE on STN

ACCESSION NUMBER: 93012891 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1398032
TITLE: Sequence and functional analysis of the cloned Neisseria meningitidis CMP-NeuNAc synthetase.
AUTHOR: Edwards U; Frosch M
CORPORATE SOURCE: Institut fur Medizinische Mikrobiologie, Medizinische Hochschule Hannover, FRG.

Searcher : Shears 571-272-2528

SOURCE: FEMS microbiology letters, (1992 Sep 15) 75 (2-3) 161-6.
Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M95053
ENTRY MONTH: 199211
ENTRY DATE: Entered STN: 19930122
Last Updated on STN: 19980206
Entered Medline: 19921119

AB The CMP-N-acetylneuraminic acid (CMP-NeuNAc) synthetase gene of **Neisseria meningitidis** group B is located on a 2.3-kb EcoRI fragment within the cps gene cluster. **Nucleotide** sequence **determination** of the gene encoding the CMP-NeuNAc synthetase revealed a 515-bp **open reading frame** that can encode a 18.9-kDA **protein.** A computer data base scan revealed a 59.4% identity to the CMP-NeuNAc synthetase gene of E. coli K1. Enzymatic activity was confirmed in vitro and in vivo. Transformation of the CMP-NeuNAc defective E. coli K1 strain EV5 with the **meningococcal** CMP-NeuNAc synthetase could complement the defect in E. coli.

L6 ANSWER 24 OF 26 MEDLINE on STN DUPLICATE 18
ACCESSION NUMBER: 92261288 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1813777
TITLE: Cloning and expression in Escherichia coli of opc, the gene for an unusual class 5 outer membrane protein from Neisseria meningitidis (meningococci/surface antigen).
AUTHOR: Olyhoek A J; Sarkari J; Bopp M; Morelli G; Achtman M
CORPORATE SOURCE: Max-Planck Institut fur molekulare Genetik, Berlin, Germany.
SOURCE: Microbial pathogenesis, (1991 Oct) 11 (4) 249-57.
Journal code: 8606191. ISSN: 0882-4010.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M80195; GENBANK-S72518; GENBANK-S72520; GENBANK-S78944; GENBANK-S78945; GENBANK-S78946; GENBANK-S78947; GENBANK-S78948; GENBANK-S78949; GENBANK-S78950
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920626
Last Updated on STN: 19950206
Entered Medline: 19920616

AB A genomic library was constructed in a lambda gt11 vector using chromosomal DNA from a **meningococcal** serogroup A strain and plaques expressing the class 5C **protein** were recognized by **screening** with specific monoclonal antibodies. The opc insert was subcloned into a multicopy plasmid which induced expression of that **protein** in Escherichia coli as a surface-exposed major outer membrane **protein.** The **nucleotide** sequence of opc is typical of an outer membrane **protein** with a promoter and terminator region, a leader **peptide** which is cleaved during expression and a complete **open reading frame.** Unlike other **meningococcal** class 5 **proteins** or gonococcal P.II **proteins,** the

sequence did not contain any pentanucleotide repeats and the sequence showed little homology to these other functionally related **proteins**. However, the predicted **amino** acid sequence of the mature **protein** for opc showed 27% similarity to that for a second opa gene cloned from the same **meningococcal** strain. This is the first report of cloning and expression of a functional **meningococcal** gene encoding a class 5 outer membrane **protein** in E. coli.

L6 ANSWER 25 OF 26 MEDLINE on STN DUPLICATE 19
ACCESSION NUMBER: 91119408 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1703755
TITLE: cDNA and derived amino acid sequence of rabbit nasal cytochrome P450NMb (P450IIG1), a unique isozyme possibly involved in olfaction.
AUTHOR: Ding X X; Porter T D; Peng H M; Coon M J
CORPORATE SOURCE: Department of Biological Chemistry, Medical School, University of Michigan, Ann Arbor 48109-0606.
CONTRACT NUMBER: DK-10339 (NIDDK)
SOURCE: Archives of biochemistry and biophysics, (1991 Feb 15) 285 (1) 120-5.
Journal code: 0372430. ISSN: 0003-9861.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199103
ENTRY DATE: Entered STN: 19910329
Last Updated on STN: 19960129
Entered Medline: 19910306

AB Olfactory-specific cytochrome P450NMb was previously purified to electrophoretic homogeneity from microsomes of rabbit nasal mucosa in this laboratory. In the present study, a cDNA library made from poly(A)+ RNA from rabbit nasal mucosa was **screened** with antibodies to this P450, and eight immunopositive clones were isolated and characterized. The sequence **determined** from two overlapping clones contained an **open reading frame** of 1446 **nucleotides**, with the predicted first 39 **amino** acids corresponding to residues 12 to 50 of purified **NMb**, except for position 46, where Leu was encoded instead of the Glu residue that was found earlier by Edman degradation analysis. The complete **polypeptide**, including residues 1 to 11, contains 494 **amino** acid residues and has a molecular weight of 56,640. Sequence comparisons indicated that **NMb** is more than 50% identical to members of the rabbit P450 gene II family, including IIB4, IIC3, IIC5, IIE1, and IIE2, and 83% identical to rat P450olf1 (IIG1). Hybridization of **NMb** to electrophoretically fractionated rabbit nasal poly(A)+ RNA revealed 3.6- and 2.1-kb species, but with a probe derived from the 3'-nontranslated portion of the cDNA only the 3.6-kb band was observed, suggesting the use of alternate polyadenylation sites or splicing. In agreement with the known tissue-specific distribution of **NMb protein**, **NMb** transcripts were found in olfactory mucosa, but not in liver, lung, intestine, or kidney. Genomic hybridization analysis indicated that there may be only one copy of the **NMb** gene present in the rabbit genome.

L6 ANSWER 26 OF 26 MEDLINE on STN DUPLICATE 20
ACCESSION NUMBER: 89343617 MEDLINE

DOCUMENT NUMBER: PubMed ID: 2503673
TITLE: The class 1 outer membrane protein of Neisseria meningitidis: gene sequence and structural and immunological similarities to gonococcal porins.
AUTHOR: Barlow A K; Heckels J E; Clarke I N
CORPORATE SOURCE: Department of Microbiology, University of Southampton Medical School, UK.
SOURCE: Molecular microbiology, (1989 Feb) 3 (2) 131-9. Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X12899
ENTRY MONTH: 198909
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890911

AB The class 1 **protein** is a major **protein** of the outer membrane of **Neisseria meningitidis**, and an important immunodeterminant in humans. The complete **nucleotide** sequence for the structural gene of a class 1 **protein** has been **determined**. The sequence predicts a **protein** of 374 **amino** acids, preceded by a typical signal **peptide** of 19 residues. The hydropathy profile of the predicted **protein** sequence resembles that of the Escherichia coli and gonococcal porins. The predicted **protein** sequence of the class 1 **protein** exhibits considerable structural similarity to the gonococcal porins PIA and PIB. Western blot studies also reveal immunologically conserved domains between the class 1 **protein**, PIA and PIB. A restriction fragment from the class 1 gene hybridizes to gonococcal genomic fragments in Southern blots. In addition to the class 1 gene coding region there is a large **open reading frame** on the opposite strand.

Searcher : Shears 571-272-2528

>>> USPATFULL and USPAT2 can be accessed and searched together <<<
>>> through the new cluster USPATALL. Type FILE USPATALL to <<<
>>> enter this cluster. <<<
>>> <<<
>>> Use USPATALL when searching terms such as patent assignees, <<<
>>> classifications, or claims, that may potentially change from <<<
>>> the earliest to the latest publication. <<<

This file contains CAS Registry Numbers for easy and accurate substance identification.

L7 139 SEA FILE=USPATFULL ABB=ON PLU=ON (ORF OR OPEN READ? FRAME OR PROTEIN CODING SEQUENC?)(S)(NMB(S)(MENINGIT? OR MENINGOCOCC?) OR (NEISSER? OR N)(W)MENINGITID? OR MENINGOCOCC?)
L8 85 SEA FILE=USPATFULL ABB=ON PLU=ON L7(S)(IDENTIF? OR DETERM? OR DETECT? OR DET## OR SCREEN?)
L9 20 SEA FILE=USPATFULL ABB=ON PLU=ON L8(S)NUCLEOTIDE
L10 17 SEA FILE=USPATFULL ABB=ON PLU=ON L9(S)(AMINO OR PROTEIN OR POLYPROTEIN OR PEPTIDE OR POLYPEPTIDE)

L10 ANSWER 1 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2005:112372 USPATFULL
TITLE: Full-length human cDNAs encoding potentially secreted proteins
INVENTOR(S): Dumas Milne Edwards, Jean-Baptiste, Paris, FRANCE
Bougueleret, Lydie, Petit Lancy, SWITZERLAND
Jobert, Severin, Paris, FRANCE

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2005096458	A1	20050505
APPLICATION INFO.:	US 2003-643836	A1	20030819 (10)

RELATED APPLN. INFO.: Division of Ser. No. US 2000-731872, filed on 7 Dec 2000, ABANDONED

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-169629P	19991208 (60)
	US 2000-187470P	20000306 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SALIWANCHIK LLOYD & SALIWANCHIK, A PROFESSIONAL ASSOCIATION, PO BOX 142950, GAINESVILLE, FL, 32614-2950, US
NUMBER OF CLAIMS: 16
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Page(s)
LINE COUNT: 28075
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention concerns GENSET polynucleotides and polypeptides. Such GENSET products may be used as reagents in forensic analyses, as chromosome markers, as tissue/cell/organelle-specific markers, in the production of expression vectors. In addition, they may be used in screening and diagnosis assays for abnormal GENSET expression and/or biological activity and for screening compounds that may be used in the treatment of GENSET-related disorders.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 530/350.000
INCLS: 514/012.000; 435/069.100; 435/320.100; 435/325.000; 536/023.500
NCL NCLM: 530/350.000

L10 ANSWER 2 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2005:111614 USPATFULL
TITLE: SELECTED NUCLEOTIDE SEQUENCES ISOLATED FROM PATHOGENIC STRAINS OF HAEMOPHILUS INFLUENZAE
INVENTOR(S): Ehrlich, Garth D., Pittsburgh, PA, UNITED STATES
Antalis, Patricia, Sewickley, PA, UNITED STATES
Gladitz, John, Pittsburgh, PA, UNITED STATES
Erdos, Geza, Wexford, PA, UNITED STATES
Hu, Fen Z., Pittsburgh, PA, UNITED STATES
PATENT ASSIGNEE(S): Allegheny-Singer Research Institute (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2005095693	A1	20050505
APPLICATION INFO.:	US 2003-698235	A1	20031031 (10)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Ansel M. Schwartz, Suite 304, 201 N. Craig Street, Pittsburgh, PA, 15213, US
NUMBER OF CLAIMS: 2
EXEMPLARY CLAIM: 1
LINE COUNT: 1639
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A DNA sequence of Haemophilus influenzae clone 151_04 shown in SEQ. ID. NO. 1. A DNA sequence of Haemophilus influenzae clone 125_L2 shown in SEQ. ID. NO. 2. A DNA sequence of Haemophilus influenzae clone 179_D14 shown in SEQ. ID. NO. 3. A DNA sequence of Haemophilus influenzae clone 167_A16 shown in SEQ. ID. NO. 4.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 435/252.300
INCLS: 536/023.700
NCL NCLM: 435/252.300
NCLS: 536/023.700

L10 ANSWER 3 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2005:86996 USPATFULL
TITLE: Omp85 proteins of neisseria gonorrhoeae and neisseria meningitidis, compositions containing same and methods of use thereof
INVENTOR(S): Judd, Ralph C., Florence, MT, UNITED STATES
Manning, D. Scott, Missoula, MT, UNITED STATES
PATENT ASSIGNEE(S): The University of Montana, Missoula, MT, UNITED STATES (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2005074458	A1	20050407
APPLICATION INFO.:	US 2003-606618	A1	20030626 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 2001-994192, filed on 26 Nov 2001, GRANTED, Pat. No. US 6610306
Continuation of Ser. No. US 1998-177039, filed on

22 Oct 1998, ABANDONED
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: HOWSON AND HOWSON, ONE SPRING HOUSE CORPORATION CENTER, BOX 457, 321 NORRISTOWN ROAD, SPRING HOUSE, PA, 19477
NUMBER OF CLAIMS: 19
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 10 Drawing Page(s)
LINE COUNT: 2566
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Nucleic acid and amino acid sequences of the Omp85 proteins of N. gonorrhoeae and N. meningitidis, and fragments thereof are useful in vaccine compositions, therapeutic compositions and diagnostic compositions for use in the prevention, treatment and diagnosis of non-symptomatic gonococcal infection or symptomatic disease and non-symptomatic meningococcal infection and symptomatic disease. Antibodies are developed to these proteins and also useful in the compositions and methods described herein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 424/184.100
NCL NCLM: 424/184.100

L10 ANSWER 4 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2004:63362 USPATFULL
TITLE: Component for vaccine
INVENTOR(S): De Bolle, Xavier Thomas, Namur, BELGIUM
Letesson, Jean-Jacques, Namur, BELGIUM
Lobet, Yves, Rixensart, BELGIUM
Mertens, Pascal Yvon, Namur, BELGIUM
Poolman, Jan, Rixensart, BELGIUM
Voet, Pierre, Rixensart, BELGIUM

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004047880	A1	20040311	
APPLICATION INFO.:	US 2003-398104	A1	20030910	(10)
	WO 2001-EP11409		20011003	

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2000-24200	20001003

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SMITHKLINE BEECHAM CORPORATION, CORPORATE INTELLECTUAL PROPERTY-US, UW2220, P. O. BOX 1539, KING OF PRUSSIA, PA, 19406-0939
NUMBER OF CLAIMS: 47
EXEMPLARY CLAIM: 1
LINE COUNT: 3643
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to a component for a vaccine against menigococci, in particular peptides which mimic epitopes of meningococcal lipooligosaccharide, and to a vaccine comprising such a component.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 424/190.100

INCLS: 514/054.000
NCL NCLM: 424/190.100
NCLS: 514/054.000

L10 ANSWER 5 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2004:24675 USPATFULL
TITLE: Listeria inocua, genome and applications
INVENTOR(S): Kunst, Frederik, Ivry Sur Seine, FRANCE
Glaser, Philippe, Paris, FRANCE

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004018514	A1	20040129	
APPLICATION INFO.:	US 2003-398221	A1	20030710	(10)
	WO 2001-FR3061		20011004	

	NUMBER	DATE
PRIORITY INFORMATION:	FR 2000-12697	20001004

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP, 1300 I STREET, NW, WASHINGTON, DC, 20005
NUMBER OF CLAIMS: 87
EXEMPLARY CLAIM: 1
LINE COUNT: 8329
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention concerns a nucleotide sequence derived from Listeria inocua corresponding to a sequence selected among SEQ ID NO: 1 to SEQ ID NO: 11 and the comparative analysis of said genome with that of Listeria monocytogenes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 435/006.000
INCLS: 536/023.700; 702/020.000; 435/252.300; 435/320.100; 514/001.000
NCL NCLM: 435/006.000
NCLS: 435/252.300; 435/320.100; 514/001.000; 536/023.700; 702/020.000

L10 ANSWER 6 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2004:12955 USPATFULL
TITLE: Novel human polynucleotides and polypeptides encoded thereby
INVENTOR(S): Leach, Martin D., Madison, CT, UNITED STATES
Shimkets, Richard A., Guilford, CT, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004009474	A1	20040115	
APPLICATION INFO.:	US 2001-864408	A1	20010524	(9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-206690P	20000524 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Ivor R. Elrifi, Esq., MIintz, Levin, Cohn, Ferris,, Glovsky and Popeo, P.C., One Financial Center,

Boston, MA, 02111
NUMBER OF CLAIMS: 32
EXEMPLARY CLAIM: 1
LINE COUNT: 21366
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides ORFX, a novel isolated polypeptide, as well as a polynucleotide encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptide, polynucleotide or antibody. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to others uses.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 435/006.000
INCLS: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000; 536/023.200
NCL NCLM: 435/006.000
NCLS: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000; 536/023.200

L10 ANSWER 7 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2003:258639 USPATFULL
TITLE: 207 human secreted proteins
INVENTOR(S): Ni, Jian, Germantown, MD, UNITED STATES
Ebner, Reinhard, Gaithersburg, MD, UNITED STATES
LaFleur, David W., Washington, DC, UNITED STATES
Moore, Paul A., Germantown, MD, UNITED STATES
Olsen, Henrik S., Gaithersburg, MD, UNITED STATES
Rosen, Craig A., Laytonsville, MD, UNITED STATES
Ruben, Steven M., Olney, MD, UNITED STATES
Soppet, Daniel R., Centreville, VA, UNITED STATES
Young, Paul E., Gaithersburg, MD, UNITED STATES
Shi, Yanggu, Gaithersburg, MD, UNITED STATES
Florence, Kimberly A., Rockville, MD, UNITED STATES
Wei, Ying-Fei, Berkeley, CA, UNITED STATES
Florence, Charles, Rockville, MD, UNITED STATES
Hu, Jing-Shan, Mountain View, CA, UNITED STATES
Li, Yi, Sunnyvale, CA, UNITED STATES
Kyaw, Hla, Frederick, MD, UNITED STATES
Fischer, Carrie L., Burke, VA, UNITED STATES
Ferrie, Ann M., Painted Post, NY, UNITED STATES
Fan, Ping, Potomac, MD, UNITED STATES
Feng, Ping, Gaithersburg, MD, UNITED STATES
Endress, Gregory A., Florence, MA, UNITED STATES
Dillon, Patrick J., Carlsbad, CA, UNITED STATES
Carter, Kenneth C., North Potomac, MD, UNITED STATES
Brewer, Laurie A., St. Paul, MN, UNITED STATES
Yu, Guo-Liang, Berkeley, CA, UNITED STATES
Zeng, Zhizhen, Lansdale, PA, UNITED STATES
Greene, John M., Gaithersburg, MD, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003181692	A1	20030925
APPLICATION INFO.:	US 2001-933767	A1	20010822 (9)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. WO 2001-US5614,

filed on 21 Feb 2001, PENDING Continuation-in-part of Ser. No. US 1998-205258, filed on 4 Dec 1998, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-184836P	20000224 (60)
	US 2000-193170P	20000329 (60)
	US 1997-48885P	19970606 (60)
	US 1997-49375P	19970606 (60)
	US 1997-48881P	19970606 (60)
	US 1997-48880P	19970606 (60)
	US 1997-48896P	19970606 (60)
	US 1997-49020P	19970606 (60)
	US 1997-48876P	19970606 (60)
	US 1997-48895P	19970606 (60)
	US 1997-48884P	19970606 (60)
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	US 1997-48971P	19970606 (60)
	US 1997-48964P	19970606 (60)
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	US 1997-57645P	19970905 (60)
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	US 1997-57584P	19970905 (60)
	US 1997-57647P	19970905 (60)
	US 1997-57661P	19970905 (60)

Searcher : Shears 571-272-2528

	US 1997-57662P	19970905 (60)
	US 1997-57646P	19970905 (60)
	US 1997-57654P	19970905 (60)
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	US 1997-57765P	19970905 (60)
	US 1997-57762P	19970905 (60)
	US 1997-57775P	19970905 (60)
	US 1997-57648P	19970905 (60)
	US 1997-57774P	19970905 (60)
	US 1997-57649P	19970905 (60)
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	US 1997-57634P	19970905 (60)
	US 1997-70923P	19971218 (60)
	US 1998-92921P	19980715 (60)
	US 1998-94657P	19980730 (60)
	US 1997-70923P	19971218 (60)
	US 1998-92921P	19980715 (60)
	US 1998-94657P	19980730 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
NUMBER OF CLAIMS: 23
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 10 Drawing Page(s)
LINE COUNT: 32746
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating diseases, disorders, and/or conditions related to these novel human secreted proteins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 536/023.100
INCLS: 530/350.000; 435/325.000; 435/183.000; 435/069.100; 435/320.100
NCL NCLM: 536/023.100
NCLS: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000

L10 ANSWER 8 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2003:219631 USPATFULL
TITLE: Full-length human cDNAs encoding potentially secreted proteins
INVENTOR(S): Dumas Milne Edwards, Jean-Baptiste, Paris, FRANCE
Bougueleret, Lydie, Petit Lancy, SWITZERLAND

Jobert, Severin, Paris, FRANCE

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003152921	A1	20030814
APPLICATION INFO.:	US 2001-876997	A1	20010608 (9)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2000-731872, filed on 7 Dec 2000, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-169629P	19991208 (60)
	US 2000-187470P	20000306 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Frank C. Eisenschenk, Ph.D., SALIWANCHIK, LLOYD & SALIWANCHIK, 2421 N.W. 41 STREET, SUITE A-1, GAINESVILLE, FL, 32606-6669
NUMBER OF CLAIMS: 22
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Page(s)
LINE COUNT: 27600
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention concerns GENSET polynucleotides and polypeptides. Such GENSET products may be used as reagents in forensic analyses, as chromosome markers, as tissue/cell/organelle-specific markers, in the production of expression vectors. In addition, they may be used in screening and diagnosis assays for abnormal GENSET expression and/or biological activity and for screening compounds that may be used in the treatment of GENSET-related disorders.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 435/006.000
INCLS: 435/183.000; 536/023.200
NCL NCLM: 435/006.000
NCLS: 435/183.000; 536/023.200

L10 ANSWER 9 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2003:152836 USPATFULL
TITLE: Two-component system that controls bacterial membrane synthesis
INVENTOR(S): Apicella, Michael A., Solon, IA, UNITED STATES
Preston, Andrew, Cambridge, UNITED KINGDOM
PATENT ASSIGNEE(S): University of Iowa Research Foundation (2)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003104502	A1	20030605
APPLICATION INFO.:	US 2002-288986	A1	20021105 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1999-439226, filed on 12 Nov 1999, GRANTED, Pat. No. US 6518037
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SCHWEGMAN, LUNDBERG, WOESSNER & KLUTH, P.A., P.O. BOX 2938, MINNEAPOLIS, MN, 55402
NUMBER OF CLAIMS: 18
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 968

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention discloses a mutant Neisseria having extensive membrane blebbing, both an indicium and a cause of virulence in the gonococcus and meningococcus. Methods are disclosed for making and characterizing the mutant, bmrRS. Methods are disclosed for isolating bmrRS membranes for use as a vaccine. Methods are also disclosed for the use of the mutant for determining the virulence of clinical samples of N. gonorrhoeae and N. meningitidis. Methods are also disclosed for the screening of antibiotics targeted to virulent Neisseria.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 435/007.320
INCLS: 435/069.300; 435/219.000; 435/252.300; 435/320.100; 536/023.200
NCL NCLM: 435/007.320
NCLS: 435/069.300; 435/219.000; 435/252.300; 435/320.100; 536/023.200

L10 ANSWER 10 OF 17 USPATFULL on STN

ACCESSION NUMBER: 2003:152336 USPATFULL

TITLE: Antigenic iron repressible proteins from N. meningitidis related to the hemolysin family of toxins

INVENTOR(S): Sparling, P. Frederick, Moncure, NC, UNITED STATES
Thompson, Stuart, Carrboro, NC, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003104002	A1	20030605
	US 6887482	B2	20050503
APPLICATION INFO.:	US 2002-193950	A1	20020710 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1998-45177, filed on 20 Mar 1998, ABANDONED Continuation-in-part of Ser. No. US 1994-323477, filed on 14 Oct 1994, GRANTED, Pat. No. US 6086896 Continuation of Ser. No. US 1992-920963, filed on 28 Jul 1992, ABANDONED Continuation-in-part of Ser. No. US 1992-895123, filed on 8 Jun 1992, ABANDONED Continuation-in-part of Ser. No. US 1990-552649, filed on 16 Jul 1990, ABANDONED

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Irving N. Feit, Esq., HOFFMANN & BARON, LLP, 6900 Jericho Turnpike, Syosset, NY, 11791
NUMBER OF CLAIMS: 62
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Page(s)
LINE COUNT: 1554

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB An isolated, antigenic polypeptide comprises a segment having at least fifty amino acid residues. The amino acid sequence of the segment is present in N. meningitidis, and is different from, but substantially homologous with, the amino acid sequence of a segment of a member of the hemolysin family of toxins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 424/190.100
INCLS: 424/250.100; 530/350.000

NCL NCLM: 424/250.100
NCL NCLM: 424/190.100
NCLS: 424/185.100; 424/190.100; 424/234.100; 424/236.100; 424/249.100; 530/350.000

L10 ANSWER 11 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2003:152333 USPATFULL
TITLE: Novel therapeutic compositions for treating infection by Lawsonia spp.
INVENTOR(S): Rosey, Everett Lee, Preston, CT, UNITED STATES
King, Kendall Wayne, Waterford, CT, UNITED STATES
Good, Robert Trygve, Romsey, AUSTRALIA
Strugnell, Richard Anthony, Hawthorn, AUSTRALIA

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003103999	A1	20030605	
	US 6846487	B2	20050125	
APPLICATION INFO.:	US 2001-10160	A1	20011109	(10)

	NUMBER	DATE
PRIORITY INFORMATION:	AU 2000-1381	20001120
	US 2000-249595P	20001117 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: KNOBBE MARTENS OLSON & BEAR LLP, 2040 MAIN STREET, FOURTEENTH FLOOR, IRVINE, CA, 92614
NUMBER OF CLAIMS: 50
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 1 Drawing Page(s)
LINE COUNT: 4819
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates generally to therapeutic compositions for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by Lawsonia intracellularis or similar or otherwise related microorganism. In particular, the present invention provides a novel gene derived from Lawsonia intracellularis, which encodes an immunogenic polypeptide that is particularly useful as an antigen in a vaccine preparation for conferring humoral immunity against Lawsonia intracellularis and related pathogens in animal hosts, wherein said polypeptide is selected from the group consisting of flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN polypeptides, or a homologue, analogue or derivative of any one or more of said polypeptides. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting Lawsonia intracellularis or similar or otherwise related microorganisms.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 424/190.100
INCLS: 530/350.000; 435/069.300; 435/252.300; 435/320.100; 536/023.200
NCL NCLM: 424/190.100
NCL NCLM: 424/190.100
NCLS: 424/184.100; 424/185.100; 424/263.100; 435/069.300; 435/252.300; 435/320.100; 530/350.000; 536/023.100; 536/023.200; 536/023.700

L10 ANSWER 12 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2002:283365 USPATFULL
TITLE: Invasion associated genes from Neisseria meningitidis serogroup B
INVENTOR(S): Ribot, Efrain M., Atlanta, GA, United States
Stephens, David S., Stone Mountain, GA, United States
Raymond, Nigel, Wellington, NEW ZEALAND
Quinn, Frederick D., Avondale Estates, GA, United States
PATENT ASSIGNEE(S): Centers for Disease Control and Prevention, as represented by the Secretary, Department of Health and Human Services, Atlanta, GA, United States (U.S. government)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6472518	B1	20021029	
	WO 9817805		19980430	
APPLICATION INFO.:	US 1999-284926		19990817	(9)
	WO 1997-US19424		19971024	
			19990817	PCT 371 date

	NUMBER	DATE
PRIORITY INFORMATION:	US 1996-30432P	19961024 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Graser, Jennifer E.
LEGAL REPRESENTATIVE: Needle & Roseberg, P.C.
NUMBER OF CLAIMS: 7
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 27 Drawing Figure(s); 27 Drawing Page(s)
LINE COUNT: 3137
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Genes isolated from Neisseria memingitidis, as well as isolated nucleic acids, probes, expression cassettes, polypeptides, antibodies, immunogenic compositions, antisense nucleic acids, amplification mixtures, and new invasion deficient swains of Neisseria meningitidis are provided Methods of detecting Neisseria meningitidis and Neisseria meningitidis nucleic acids, and methods of inhibiting the invasion of mammalian cells by Neisseria meningitidis are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 536/023.700
INCLS: 536/024.320; 536/024.330; 536/024.100; 424/250.100; 435/243.000; 435/252.300; 435/320.100; 435/069.100; 435/069.300
NCL NCLM: 536/023.700
NCLS: 424/250.100; 435/069.100; 435/069.300; 435/243.000; 435/252.300; 435/320.100; 536/024.100; 536/024.320; 536/024.330

L10 ANSWER 13 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2002:191539 USPATFULL
TITLE: Full-length human cDNAs encoding potentially secreted proteins

INVENTOR(S): Milne Edwards, Jean-Baptiste Dumas, Paris, FRANCE
Bougueleret, Lydie, Petit Lancy, SWITZERLAND
Jobert, Severin, Paris, FRANCE

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002102604	A1	20020801
APPLICATION INFO.:	US 2000-731872	A1	20001207 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-169629P	19991208 (60)
	US 2000-187470P	20000306 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: John Lucas, Ph.D., J.D., Genset Corporation, 10665 Srrento Valley Road, San Diego, CA, 92121-1609
NUMBER OF CLAIMS: 29
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Page(s)
LINE COUNT: 28061
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention concerns GENSET polynucleotides and polypeptides. Such GENSET products may be used as reagents in forensic analyses, as chromosome markers, as tissue/cell/organelle-specific markers, in the production of expression vectors. In addition, they may be used in screening and diagnosis assays for abnormal GENSET expression and/or biological activity and for screening compounds that may be used in the treatment of GENSET-related disorders.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 435/007.100
INCLS: 536/023.100; 530/350.000
NCL NCLM: 435/007.100
NCLS: 530/350.000; 536/023.100

L10 ANSWER 14 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2002:164414 USPATFULL
TITLE: Omp85 proteins of neisseria gonorrhoeae and neisseria meningitidis, compositions containing same and methods of use thereof
INVENTOR(S): Judd, Ralph C., Florence, MT, UNITED STATES
Manning, D. Scott, Missoula, MT, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002086028	A1	20020704
	US 6610306	B2	20030826
APPLICATION INFO.:	US 2001-994192	A1	20011126 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1998-177039, filed on 22 Oct 1998, PENDING
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: HOWSON AND HOWSON, ONE SPRING HOUSE CORPORATION CENTER, BOX 457, 321 NORRISTOWN ROAD, SPRING HOUSE, PA, 19477
NUMBER OF CLAIMS: 25
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 10 Drawing Page(s)

LINE COUNT: 2013
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Nucleic acid and amino acid sequences of the Omp85 proteins of N. gonorrhoeae and N. meningitidis, and fragments thereof are useful in vaccine compositions, therapeutic compositions and diagnostic compositions for use in the prevention, treatment and diagnosis of non-symptomatic gonococcal infection or symptomatic disease and non-symptomatic meningococcal infection and symptomatic disease. Antibodies are developed to these proteins and also useful in the compositions and methods described herein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 424/184.100
NCL NCLM: 424/250.100
NCL NCLM: 424/184.100
NCLS: 424/184.100; 424/190.100; 424/192.100; 424/234.100; 514/002.000; 530/350.000; 530/825.000

L10 ANSWER 15 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2001:152492 USPATFULL
TITLE: Proteinase K resistant surface protein of neisseria meningitidis
INVENTOR(S): Brodeur, Bernard R., Sillery, Canada
Martin, Denis, St-Augustin-de-Des Maures, Canada
Hamel, Josee, Sillery, Canada
Rioux, Clement, Ville-de-Cap-Rouge, Canada
PATENT ASSIGNEE(S): BioChem Pharma Inc., Quebec, Canada (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6287574	B1	20010911
APPLICATION INFO.:	US 1997-913362		19971113 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1995-406362, filed on 17 Mar 1995, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	US 1995-1983P	19950804 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Graser, Jennifer
LEGAL REPRESENTATIVE: Foley & Lardner
NUMBER OF CLAIMS: 9
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 27 Drawing Figure(s); 23 Drawing Page(s)
LINE COUNT: 2034
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A highly conserved, immunologically accessible antigen at the surface of Neisseria meningitidis organisms. Immunotherapeutic, prophylactic and diagnostic compositions and methods useful in the treatment, prevention an diagnosis of Neisseria meningitidis diseases. A proteinase K resistant Neisseria meningitidis surface protein having an apparent molecular weight of 22 kDa, the corresponding nucleotide and derived amino acid sequences (SEQ ID NO: 1, NO:3, NO:5 and NO:7: SEQ ID NO: 2, NO:4, NO:6, and NO:8), recombinant DNA methods for the production of the Neisseria meningitidis 22 kDA surface protein, and antibodies that bind to the Neisseria meningitidis 22 kDA surface protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 424/250.100
INCLS: 424/249.100; 424/184.100; 424/185.100; 424/190.100; 530/300.000; 530/350.000; 536/023.700
NCL NCLM: 424/250.100
NCLS: 424/184.100; 424/185.100; 424/190.100; 424/249.100; 530/300.000; 530/350.000; 536/023.700

L10 ANSWER 16 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2001:139307 USPATFULL
TITLE: TWO-COMPONENT SYSTEM THAT CONTROLS BACTERIAL MEMBRANE SYNTHESIS
INVENTOR(S): APICELLA, MICHAEL A., SOLON, IA, United States
PRESTON, ANDREW, CAMBRIDGE, Great Britain

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2001016349	A1	20010823
	US 6518037	B2	20030211
APPLICATION INFO.:	US 1999-439226	A1	19991112 (9)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SCHWEGMAN LUNDBERG WOESSNER & KLUTH P A, P O BOX 2938, MINNEAPOLIS, MN, 55402
NUMBER OF CLAIMS: 5
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 668
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention discloses a mutant Neisseria having extensive membrane blebbing, both an indicium and a cause of virulence in the gonococcus and meningococcus. Methods are disclosed for making and characterizing the mutant, bmrRS. Methods are disclosed for isolating bmrRS membranes for use as a vaccine. Methods are also disclosed for the use of the mutant for determining the virulence of clinical samples of N. gonorrhoeae and N. meningitidis. Methods are also disclosed for the screening of antibiotics targeted to virulent Neisseria.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 435/252.100
INCLS: 435/243.000; 435/871.000
NCL NCLM: 435/032.000
NCL NCLM: 435/252.100
NCLS: 435/006.000; 435/007.320; 435/029.000; 435/243.000; 435/871.000

L10 ANSWER 17 OF 17 USPATFULL on STN
ACCESSION NUMBER: 2000:87727 USPATFULL
TITLE: Antigenic iron repressible protein from N. meningitidis related to the hemolysin family of toxins
INVENTOR(S): Sparling, P. Frederick, Moncure, NC, United States
Thompson, Stuart, Carrboro, NC, United States
PATENT ASSIGNEE(S): ImClone Systems Incorporated, New York, NY, United States (U.S. corporation)

	NUMBER	KIND	DATE

PATENT INFORMATION:	US 6086896	20000711
APPLICATION INFO.:	US 1994-323477	19941014 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1992-920963, filed on 28 Jul 1992, now abandoned which is a continuation-in-part of Ser. No. US 1990-552649, filed on 16 Jul 1990, now abandoned

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Sidberry, Hazel F.
LEGAL REPRESENTATIVE: Hoffmann & Baron, LLP
NUMBER OF CLAIMS: 3
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 3 Drawing Figure(s); 13 Drawing Page(s)
LINE COUNT: 1271
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB An isolated, antigenic polypeptide comprises a segment having at least fifty amino acid residues. The amino acid sequence of the segment is present in N. meningitidis, and is different from, but substantially homologous with, the amino acid sequence of a segment of a member of the hemolysin family of toxins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
INCL INCLM: 424/250.100
INCLS: 424/184.100; 424/185.100; 424/249.100; 530/350.000; 435/007.100
NCL NCLM: 424/250.100
NCLS: 424/184.100; 424/185.100; 424/249.100; 435/007.100; 530/350.000

(FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, USPATFULL' ENTERED AT 14:45:26 ON 15 AUG 2005)

L11	4839	SEA	ABB=ON	PLU=ON	"FRASER C"?/AU
L12	683	SEA	ABB=ON	PLU=ON	"HICKEY E"?/AU
L13	12066	SEA	ABB=ON	PLU=ON	"PETERSON J"?/AU
L14	199	SEA	ABB=ON	PLU=ON	"TETTELIN H"?/AU
L15	2320	SEA	ABB=ON	PLU=ON	("VENTER C"? OR "VENTER J"?)/AU
L16	170	SEA	ABB=ON	PLU=ON	"MASIGNANI V"?/AU
L17	167	SEA	ABB=ON	PLU=ON	"GALEOTTI C"?/AU
L18	507	SEA	ABB=ON	PLU=ON	"RATTI G"?/AU
L19	304	SEA	ABB=ON	PLU=ON	"SCARSELLI M"?/AU
L20	326	SEA	ABB=ON	PLU=ON	"SCARLATO V"?/AU
L21	2315	SEA	ABB=ON	PLU=ON	"RAPPUOLI R"?/AU
L22	625	SEA	ABB=ON	PLU=ON	"PIZZA M"?/AU
L23	914	SEA	ABB=ON	PLU=ON	"GRANDI G"?/AU
L24	2	SEA	ABB=ON	PLU=ON	L11 AND L12 AND L13 AND L14 AND L15 AND L16 AND L17 AND L18 AND L19 AND L20 AND L21 AND L22 AND L23
L25	870	SEA	ABB=ON	PLU=ON	L11 AND (L12 OR L13 OR L14 OR L15 OR L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23)
L26	92	SEA	ABB=ON	PLU=ON	L12 AND (L13 OR L14 OR L15 OR L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23)
L27	114	SEA	ABB=ON	PLU=ON	L13 AND (L14 OR L15 OR L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23)
L28	86	SEA	ABB=ON	PLU=ON	L14 AND (L15 OR L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23)
L29	16	SEA	ABB=ON	PLU=ON	L15 AND (L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23)
L30	155	SEA	ABB=ON	PLU=ON	L16 AND (L17 OR L18 OR L19 OR L20 OR

- Author(s)

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                L21 OR L22 OR L23)
L31          37 SEA ABB=ON  PLU=ON  L17 AND (L18 OR L19 OR L20 OR L21 OR
                L22 OR L23)
L32         121 SEA ABB=ON  PLU=ON  L18 AND (L19 OR L20 OR L21 OR L22 OR
                L23)
L33          77 SEA ABB=ON  PLU=ON  L19 AND (L20 OR L21 OR L22 OR L23)
L34         214 SEA ABB=ON  PLU=ON  L20 AND (L21 OR L22 OR L23)
L35         611 SEA ABB=ON  PLU=ON  L21 AND (L22 OR L23)
L36          50 SEA ABB=ON  PLU=ON  L22 AND L23
L37          32 SEA ABB=ON  PLU=ON  (L25 OR L26 OR L27 OR L28 OR L30 OR
                L31 OR L32 OR L33 OR L34 OR L35 OR L36) AND L1
L38          43 SEA ABB=ON  PLU=ON  L24 OR L29 OR L37
L39          21 DUP REM L38 (22 DUPLICATES REMOVED)

L39  ANSWER 1 OF 21  CAPLUS  COPYRIGHT 2005 ACS on STN DUPLICATE 1
ACCESSION NUMBER:         2005:581601  CAPLUS
DOCUMENT NUMBER:          143:76811
TITLE:                    Antigen and gene sequences from Neisseria
                          meningitidis group A and B and Neisseria
                          gonorrhoeae
INVENTOR(S):              Scarlato, Vincenzo; Masignani,
                          Vega; Rappuoli, Rino; Pizza,
                          Mariagrazia; Grandi, Guido
PATENT ASSIGNEE(S):       Chiron S.r.l., Italy
SOURCE:                   U.S., 613 pp., Cont.-in-part of Appl. No.
                          PCT/IB98/01665.
                          CODEN: USXXAM
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   2
PATENT INFORMATION:

     PATENT NO.           KIND   DATE        APPLICATION NO.         DATE
     ---------------      ----   --------    --------------------    --------
     US 6914131            B1    20050705    US 1999-303518          19990430
     WO 9924578            A2    19990520    WO 1998-IB1665          19981009
     WO 9924578            A3    20000302
         W:  AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
             DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS,
             JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG,
             MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
             SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY,
             KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
             ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
             CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                   WO 1998-IB1665      A2 19981009

                                         GB 1997-23516       A  19971106

                                         GB 1997-24190       A  19971114

                                         GB 1997-24386       A  19971118

                                         GB 1997-25158       A  19971127

                                         GB 1997-26147       A  19971210

                                         GB 1998-759         A  19980114
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GB 1998-19016 A 19980901

AB The invention provides proteins from Neisseria meningitidis (strains A and B) and from Neisseria gonorrhoeae, including amino acid sequences, the corresponding nucleotide sequences, expression data, and serol. data. The proteins are useful antigens for vaccines, immunogenic compns., and/or diagnostics.

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 2 OF 21 USPATFULL on STN

ACCESSION NUMBER: 2005:24263 USPATFULL

TITLE: Streptococcus pneumoniae proteins and nucleic acids

INVENTOR(S): **Masignani, Vega**, Siena, ITALY
Tettelin, Herve, Rockville, MD, UNITED STATES
Fraser, Claire, Potomac, MD, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2005020813	A1	20050127	
APPLICATION INFO.:	US 2004-472928	A1	20040820	(10)
	WO 2002-IB2163		20020327	

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2001-7658	20010327

DOCUMENT TYPE: Utility

FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: Rebecca Hale, Chiron Corporation, Intellectual Property R338, PO Box 8097, Emeryville, CA, 94662-8097

NUMBER OF CLAIMS: 25

EXEMPLARY CLAIM: 1

LINE COUNT: 3720

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention provides proteins and nucleic acid sequences from Streptococcus pneumoniae, together with a genome sequence. These are useful for the development of vaccines, diagnostics, and antibiotics.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L39 ANSWER 3 OF 21 USPATFULL on STN

ACCESSION NUMBER: 2004:164905 USPATFULL

TITLE: Meningococcal antigens

INVENTOR(S): **Scarlato, Vincenzo**, Siena, ITALY
Masignani, Vega, Siena, ITALY
Rappuoli, Rino, Siena, ITALY
Pizza, Mariagrazia, Siena, ITALY
Grandi, Guido, Siena, ITALY

PATENT ASSIGNEE(S): Chiron S.P.A. (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004126391	A1	20040701

APPLICATION INFO.: US 2003-695499 A1 20031028 (10)
RELATED APPLN. INFO.: Continuation of Ser. No. US 1999-302626, filed on 30 Apr 1999, GRANTED, Pat. No. US 6709660 Continuation-in-part of Ser. No. WO 1999-IB103, filed on 14 Jan 1999, UNKNOWN

	NUMBER	DATE
PRIORITY INFORMATION:	GB 1998-760	19980114
	GB 1998-19015	19980901
	GB 1998-22143	19981009

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Chiron Corporation, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA, 94662-8097
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 15 Drawing Page(s)
LINE COUNT: 12723
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides proteins from Neissena meningitidis (strains A & B), including amino acid sequences, the corresponding nucleotide sequences, expression data, and serological data. The proteins are useful antigens for vaccines, immunogenic compositions, and/or diagnostics.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L39 ANSWER 4 OF 21 USPATFULL on STN
ACCESSION NUMBER: 2004:144998 USPATFULL
TITLE: Heterologous expression of neisserial proteins
INVENTOR(S): Arico, Maria Beatrice, Siena, ITALY
Comanducci, Maurizio, Siena, ITALY
Galeotti, Cesira, Montegriggioni, ITALY
Masignani, Vega, Siena, ITALY
Guiliani, Marizia Monica, Siena, ITALY
Pizza, Mariagrazia, Siena, ITALY

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004110670	A1	20040610	
APPLICATION INFO.:	US 2003-220481	A1	20030813	(10)
	WO 2001-IB452		20010228	

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2000-4695	20000228
	GB 2000-27675	20001113

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Alisa A Harbin, Chiron Corporation, Intellectual Property-R338, P O Box 8097, Emeryville, CA, 94662-8097
NUMBER OF CLAIMS: 52
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Page(s)
LINE COUNT: 5781
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Alternative and improved approaches to the heterologous expression

of the proteins of Neisseria meningitidis and Neisseria gonorrhoeae. These approaches typically affect the level of expression, the ease of purification, the cellular localisation, and/or the immunological properties of the expressed protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L39 ANSWER 5 OF 21 USPATFULL on STN
ACCESSION NUMBER: 2004:121295 USPATFULL
TITLE: Hybrid expression of neisserial proteins
INVENTOR(S): Arico, Maria Beatrice, Siena, ITALY
Comanducci, Maurizio, Siena, ITALY
Galeotti, Cesira, Montegriggioni, ITALY
Masignani, Vega, Siena, ITALY
Guiliani, Marizia Monica, Siena, ITALY
Pizza, Mariagrazia, Siena, ITALY

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004092711	A1	20040513	
APPLICATION INFO.:	US 2003-220480	A1	20030519	(10)
	WO 2001-IB420		20010228	

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2000-4695	20000228
	GB 2000-27675	20001113

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Alisa A Harbin, Chiron Corporation, Intellectual Property R338, PO Box 8097, Emeryville, CA, 94662-8097
NUMBER OF CLAIMS: 28
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Page(s)
LINE COUNT: 7849
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Two or more Neisserial proteins (e.g. A and B) are expressed as a single hybrid protein which can be represented simply by the formula NH.sub.2-A-B--COOH.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L39 ANSWER 6 OF 21 USPATFULL on STN
ACCESSION NUMBER: 2004:72507 USPATFULL
TITLE: Meningococcal antigens
INVENTOR(S): **Scarlato, Vincenzo**, Siena, ITALY
Masignani, Vega, Siena, ITALY
Rappuoli, Rino, Siena, ITALY
Pizza, Mariagrazia, Siena, ITALY
Grandi, Guido, Siena, ITALY
PATENT ASSIGNEE(S): Chrion S.r.l., Siena, ITALY (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6709660	B1	20040323	
APPLICATION INFO.:	US 1999-302626		19990430	(9)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. WO 1999-IB103, filed on 14 Jan 1999			

	NUMBER	DATE
PRIORITY INFORMATION:	GB 1998-760	19980114
	GB 1998-19015	19980901
	GB 1998-22143	19981009

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Graser, Jennifer E.
LEGAL REPRESENTATIVE: Robins, Roberta L., Harbin, Alisa A., Blackburn, Robert P.
NUMBER OF CLAIMS: 9
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 19 Drawing Figure(s); 8 Drawing Page(s)
LINE COUNT: 11904
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention provides proteins from Neisseria meningitidis (strains A & B), including amino acid sequences, the corresponding nucleotide sequences, expression data, and serological data. The proteins are useful antigens for vaccines, immunogenic compositions, and/or diagnostics.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L39 ANSWER 7 OF 21 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:556213 BIOSIS
DOCUMENT NUMBER: PREV200300556936
TITLE: Comparative genomics of Neisseria species.
AUTHOR(S): Hotopp, J. C. Dunning [Reprint Author]; Grifantini, R.; Frigimelica, E.; Draghi, M.; Giuliani, M.; **Grandi, G.**; Peterson, S. [Reprint Author]; **Tettelin, H.** [Reprint Author]
CORPORATE SOURCE: Institute for Genomic Research, Rockville, MD, USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. R-053. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
ISSN: 1060-2011 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Nov 2003
Last Updated on STN: 26 Nov 2003

AB The genus Neisseria includes pathogenic organisms (e.g. **Neisseria meningitidis** and Neisseria gonorrhoeae) as well as commensal organisms (e.g. Neisseria lactamica and Neisseria cinerea). The sequencing of two **N. meningitidis** strains and microarray technology allows for the high-throughput examination of the genomic differences between these organisms. Additionally, serotypes of **Neisseria meningitidis** can be examined for similarities and differences. Comparative genome hybridization (CGH) experiments were carried out on microarray slides containing 200-1000 bp amplicons of 97% of the **open reading frames** in **N. meningitidis** MC58. The gene differences relative to MC58 were examined in species

as distantly related as N. gonorrhoeae and N. lactamica. N. cinerea DNA was hybridized but could not be normalized thus defining a lower limit to the homology required for successful analysis. The results of the hybridizations are used to define putative pathogen-specific and meningitidis-specific subsets of genes. In addition to cross-species comparisons, a variety of serotypes of **N. meningitidis** were hybridized to the array. Other than the capsule locus and two small repeat associated regions, only minor differences were observed between the serotypes tested. More differences existed between some serotype B strains than when comparing some serotype B strains to serotype A strains. Strains from both disease cases and healthy carriers were included in this study, and as expected of an opportunistic pathogen, no significant differences were found between strains from carriers and cases. Overall, diversity could be seen throughout the entire chromosome with some islands of diversity seen in and around the putative islands of horizontal transfer identified in the sequencing of **N. meningitidis** MC58. Many single **open reading frames** are also absent in strains examined. CGH studies in other organisms to date have shown predominantly islands of variation with very few variable single **open reading frames.** This may be unique to Neisseria species and will be further examined.

L39 ANSWER 8 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:906293 CAPLUS
DOCUMENT NUMBER: 138:8311
TITLE: Staphylococcus aureus proteins and nucleic acids and their diagnostic and therapeutic uses for staphylococcal infections
INVENTOR(S): Masignani, Vega; Mora, Marirosa; Scarselli, Maria
PATENT ASSIGNEE(S): Chiron Spa, Italy
SOURCE: PCT Int. Appl., 49 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002094868	A2	20021128	WO 2002-IB2637	20020327
WO 2002094868	A3	20030918		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2440368	AA	20021128	CA 2002-2440368	20020327
EP 1373310	A2	20040102	EP 2002-749141	20020327
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2005502326	T2	20050127	JP 2002-592342	20020327
PRIORITY APPLN. INFO.:			GB 2001-7661 A	20010327

WO 2002-IB2637 W 20020327

AB The invention provides 2821 nucleic acid coding sequences from Staphylococcus aureus strain NCTC 8325 along with their inferred translation products. The proteins are useful for vaccines, immunogenic compns., diagnostics, enzymic studies, and also as targets for antibiotics.

L39 ANSWER 9 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2001:545516 CAPLUS
DOCUMENT NUMBER: 135:136409
TITLE: Outer membrane vesicle (OMV) vaccine comprising N. meningitidis serogroup B outer membrane proteins
INVENTOR(S): **Pizza, Mariagrazia; Rappuoli, Rino**; Giuliani, Marzia
PATENT ASSIGNEE(S): Chiron S.p.A., Italy
SOURCE: PCT Int. Appl., 81 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001052885	A1	20010726	WO 2001-IB166	20010117
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2397508	AA	20010726	CA 2001-2397508	20010117
EP 1248647	A1	20021016	EP 2001-942562	20010117
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2003520248	T2	20030702	JP 2001-552932	20010117
NZ 520466	A	20030926	NZ 2001-520466	20010117
BR 2001007679	A	20040706	BR 2001-7679	20010117
US 2004249125	A1	20041209	US 2003-181600	20030331

PRIORITY APPLN. INFO.:
GB 2000-1067 A 20000117
GB 2000-5699 A 20000309
WO 2001-IB166 W 20010117

AB A composition comprising (a) Neisseria meningitidis serogroup B outer membrane vesicles (OMVs), and (b) an immunogenic component selected from other Neisseria proteins, or immunogenic fragments thereof. Component (b) preferably includes a protein from a different NmB strain from that from which the OMV of component (a) is derived. The OMVs are preferably obtained by deoxycholate extn. Optionally, the compn. may also comprise a protective antigen against other pathogens.
REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR

THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 10 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:661631 CAPLUS
DOCUMENT NUMBER: 135:237577
TITLE: Manufacture of proteins of Neisseria as fusion proteins without the use of non-Neisseria sequences
INVENTOR(S): Arico, Maria Beatrice; Comanducci, Maurizio; **Galeotti, Cesira; Masignani, Vega**; Giuliani, Marzia Monica; **Pizza, Mariagrazia**
PATENT ASSIGNEE(S): Chiron S.p.A., Italy
SOURCE: PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001064920	A2	20010907	WO 2001-IB420	20010228
WO 2001064920	A3	20020314		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2400562	AA	20010907	CA 2001-2400562	20010228
EP 1261723	A2	20021204	EP 2001-914098	20010228
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2003525049	T2	20030826	JP 2001-563609	20010228
BR 2001008713	A	20040622	BR 2001-8713	20010228
NZ 521396	A	20040625	NZ 2001-521396	20010228
CN 1508253	A	20040630	CN 2003-10103603	20010228
CN 1544462	A	20041110	CN 2003-10102845	20010228
US 2004092711	A1	20040513	US 2003-220480	20030519
PRIORITY APPLN. INFO.:			GB 2000-4695 A	20000228
			GB 2000-27675 A	20001113
			WO 2001-IB420 W	20010228

AB The manufacture of **open reading frame** proteins of Neisseria (**N. meningitidis** or N. gonorrhoeae) as fusion proteins is using Escherichia coli as the expression host described. Preferably, the fusion proteins do not have any non-Neisserial proteins, such as hexahistidine or glutathione-S-transferase moieties. The removal of polyglycine tracts from the proteins greatly increases yields of the fusion products. Preparation of a number of chimeric genes and the corresponding proteins using

Escherichia coli as expression host is described.

L39 ANSWER 11 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:396693 CAPLUS
DOCUMENT NUMBER: 135:32728
TITLE: Compositions comprising Neisseria meningitidis antigens from serogroups B and C
INVENTOR(S): Giuliani, Marzia Monica; **Pizza, Mariagrazia; Rappuoli, Rino**
PATENT ASSIGNEE(S): Chiron Spa, Italy
SOURCE: PCT Int. Appl., 27 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001037863	A2	20010531	WO 2000-IB1940	20001129
WO 2001037863	A3	20011227		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2392880	AA	20010531	CA 2000-2392880	20001129
EP 1235589	A2	20020904	EP 2000-981554	20001129
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
BR 2000015958	A	20030225	BR 2000-15958	20001129
JP 2003514868	T2	20030422	JP 2001-539477	20001129
NZ 519608	A	20031128	NZ 2000-519608	20001129
CN 1507916	A	20040630	CN 2003-10104674	20001129
NZ 529213	A	20050324	NZ 2000-529213	20001129
US 2005074450	A1	20050407	US 2003-148533	20030310
PRIORITY APPLN. INFO.:			GB 1999-28196 A	19991129
			WO 2000-IB1940 W	20001129

AB International patent application WO99/61053 discloses immunogenic compns. that comprise N. meningitidis serogroup C oligosaccharide conjugated to a carrier, in combination with N. meningitidis serogroup B outer membrane protein. These are disclosed in the present application in combination with further Neisserial proteins and/or protective antigens against other pathogenic organisms (e.g. Haemophilus influenzae, DTP, HBV, etc.).

L39 ANSWER 12 OF 21 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2001-081052 [09] WPIDS
DOC. NO. NON-CPI: N2001-061729
DOC. NO. CPI: C2001-023407
TITLE: New antigenic protein fragments from Neisseria menigitidis, useful for treating, preventing and/or

diagnosing Neisserial bacterial infections.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): **GALEOTTI, C; MASIGNANI, V;** MORA, M; **SCARLATO, V; SCARSELLI, M**

PATENT ASSIGNEE(S): (CHIR) CHIRON SPA; (CHIR-N) CHIRON SPA; (CHIR) CHIRON SRL

COUNTRY COUNT: 95

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001004316	A2	20010118	(200109)*	EN	79
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000058393	A	20010130	(200127)		
EP 1196587	A2	20020417	(200233)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
BR 2000012424	A	20020702	(200252)		
CN 1373805	A	20021009	(200309)		
JP 2003504062	W	20030204	(200320)		121
MX 2002000463	A1	20030701	(200366)		
RU 2253678	C2	20050610	(200540)		
CN 1590404	A	20050309	(200542)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001004316	A2	WO 2000-IB1026	20000713
AU 2000058393	A	AU 2000-58393	20000713
EP 1196587	A2	EP 2000-944161	20000713
		WO 2000-IB1026	20000713
BR 2000012424	A	BR 2000-12424	20000713
		WO 2000-IB1026	20000713
CN 1373805	A	CN 2000-812746	20000713
JP 2003504062	W	WO 2000-IB1026	20000713
		JP 2001-509520	20000713
MX 2002000463	A1	WO 2000-IB1026	20000713
		MX 2002-463	20020114
RU 2253678	C2	WO 2000-IB1026	20000713
		RU 2002-103604	20000713
CN 1590404	A Div ex	CN 2000-812746	20000713
		CN 2004-48988	20000713

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000058393	A Based on	WO 2001004316
EP 1196587	A2 Based on	WO 2001004316
BR 2000012424	A Based on	WO 2001004316
JP 2003504062	W Based on	WO 2001004316
MX 2002000463	A1 Based on	WO 2001004316
RU 2253678	C2 Based on	WO 2001004316

Searcher : Shears 571-272-2528

PRIORITY APPLN. INFO: GB 1999-16529 19990714
AN 2001-081052 [09] WPIDS
AB WO 200104316 A UPAB: 20040907
NOVELTY - A fragment (I) of a protein from **Neisseria Meningitidis** previously disclosed in patent WO99/36544, which comprises at least 1 antigenic determinant, is new.
DETAILED DESCRIPTION - A fragment of a protein (I) from **Neisseria Meningitidis** previously disclosed in patent WO99/36544, such as amino acids 6-14, 57-59, 67-76 and 92-100 of ORF38-1 (**open reading frame** 38-1), which comprises at least 1 antigenic determinant, is new.
INDEPENDENT CLAIMS are also included for the following:
(1) a polypeptide (II) with 50% or more sequence identity to (I);
(2) a protein (III) comprising 1 or more (I), but is not 1 of the 45 complete protein sequences disclosed in WO99/36544;
(3) an antibody (IV) which recognizes (I); and
(4) a nucleic acid (V) encoding (I), (II) or (III).
ACTIVITY - Antibacterial. No supporting data is given.
MECHANISM OF ACTION - Vaccine; gene therapy.
USE - (I), a protein comprising one or more (I), a polypeptide with 50% or more sequence identity to (I), a nucleic acid encoding (I) and/or an antibody immunospecific for (I) are useful:
(1) in the manufacture of a medicament for treating or preventing infection due to Neisserial bacteria, especially Neisseria menigitidis, preferably strains A or B;
(2) as a diagnostic reagent for detecting the presence of Neisserial bacteria or antibodies immunospecific for them; and/or
(3) as a reagent which can raise antibodies against Neisserial bacteria.
These compounds are also useful for treating a patient, preferably to prevent or treat Neisserial bacterial infections (claimed).
Dwg.0/0

L39 ANSWER 13 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 2001:240640 CAPLUS
DOCUMENT NUMBER: 135:2651
TITLE: Mu-like prophage in serogroup B Neisseria meningitidis coding for surface-exposed antigens
AUTHOR(S): **Masignani, Vega**; Giuliani, Marzia Monica; **Tettelin, Herve**; Comanducci, Maurizio; **Rappuoli, Rino**; **Scarlato, Vincenzo**
CORPORATE SOURCE: Department of Molecular Biology, IRIS, Chiron S.p.A., Siena, 53100, Italy
SOURCE: Infection and Immunity (2001), 69(4), 2580-2588
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Sequence anal. of the genome of N. meningititidis serogroup B revealed the presence of an .apprx.35-kb region inserted within a putative gene coding for an ABC-type transporter. The region contains 46 **open reading frames**, 29 of which are colinear and homologous to the genes of Escherichia coli Mu phage. Two prophages with similar organizations were also found in serogroup A **meningococcus**, and one was found in Haemophilus influenzae. Early and late phage functions are well preserved in this

family of Mu-like prophages. Several regions of atypical nucleotide content were identified. These likely represent genes acquired by horizontal transfer. Three of the acquired genes are shown to code for surface-associated antigens, and the encoded proteins are able to induce bactericidal antibodies.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 14 OF 21 MEDLINE on STN
ACCESSION NUMBER: 2000175756 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10710308
TITLE: Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing.
COMMENT: Comment on: Science. 2000 Mar 10;287(5459):1767-8. PubMed ID: 10755929
AUTHOR: **Pizza M; Scarlato V; Masignani V**; Giuliani M M; Arico B; Comanducci M; Jennings G T; Baldi L; Bartolini E; Capecchi B; **Galeotti C L**; Luzzi E; Manetti R; Marchetti E; Mora M; Nuti S; **Ratti G**; Santini L; Savino S; **Scarselli M**; Storni E; Zuo P; Broeker M; Hundt E; Knapp B; Blair E; Mason T; Tettelin H; Hood D W; Jeffries A C; Saunders N J; Granoff D M; **Venter J C**; Moxon E R; **Grandi G; Rappuoli R**
CORPORATE SOURCE: IRIS, Chiron S.p.A., Via Fiorentina 1, 53100 Siena, Italy.
SOURCE: Science, (2000 Mar 10) 287 (5459) 1816-20. Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Commentary
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000403

AB Neisseria meningitidis is a major cause of bacterial septicemia and meningitis. Sequence variation of surface-exposed proteins and cross-reactivity of the serogroup B capsular polysaccharide with human tissues have hampered efforts to develop a successful vaccine. To overcome these obstacles, the entire genome sequence of a virulent serogroup B strain (MC58) was used to identify vaccine candidates. A total of 350 candidate antigens were expressed in Escherichia coli, purified, and used to immunize mice. The sera allowed the identification of proteins that are surface exposed, that are conserved in sequence across a range of strains, and that induce a bactericidal antibody response, a property known to correlate with vaccine efficacy in humans.

L39 ANSWER 15 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2000:790687 CAPLUS
DOCUMENT NUMBER: 133:359806
TITLE: **Neisseria meningitidis** B genome sequence and **open reading frames** and their diagnostic and therapeutic uses

INVENTOR(S): **Pizza, Mariagrazia; Hickey, Erin ; Peterson, Jeremy; Tettelin, Herve; Venter, J. Craig; Masignani, Vega; Galeotti, Cesira** ; Mora, Marirosa; **Ratti, Giulio; Scarselli, Maria; Scarlato, Vincenzo; Rappuoli, Rino;** Frazer, Claire M.; **Grandi, Guido**

PATENT ASSIGNEE(S): Chiron Corporation, USA; The Institute for Genomic Research

SOURCE: PCT Int. Appl., 692 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 5

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000066791	A1	20001109	WO 2000-US5928	20000308
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2000022430	A2	20000420	WO 1999-US23573	19991008
WO 2000022430	A3	20020606		
WO 2000022430	C2	20020704		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1559795	A2	20050803	EP 2005-75407	19991008
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY				
CA 2371032	AA	20001109	CA 2000-2371032	20000308
EP 1185691	A1	20020313	EP 2000-910392	20000308
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 2000010361	A	20030610	BR 2000-10361	20000308
JP 2003527079	T2	20030916	JP 2000-615413	20000308
RU 2233328	C2	20040727	RU 2001-132325	20000308
AU 780308	B2	20050317	AU 2000-32492	20000308
PRIORITY APPLN. INFO.:			US 1999-132068P	P 19990430
			WO 1999-US23573	W 19991008
			GB 2000-4695	A 20000228
			US 1998-103794P	P 19981009

Searcher : Shears 571-272-2528

EP 1999-970470 A3 19991008

WO 2000-US5928 W 20000308

AB The invention provides methods of obtaining immunogenic proteins from genomic sequences including Neisseria , including the amino acid sequences and the corresponding nucleotide sequences, as well as the full-length genomic sequence of **Neisseria meningitidis** B (strain 2996). A listing of 2158 **open reading frames** contained within the full-length sequence is also provided. **Open reading frames** (**ORFs**) 919, 279, 576-1, 519-1, 121-1, 128-1, 206, 287, and 406 are cloned and expressed in Escherichia coli. The proteins so obtained are useful antigens for vaccines, immunogenic compns., and/or diagnostics.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 16 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 5

ACCESSION NUMBER: 2000:260706 CAPLUS

DOCUMENT NUMBER: 132:304301

TITLE: Neisseria meningitidis B genomic sequences and their diagnostic and therapeutic uses

INVENTOR(S): Frazer, Claire M.; **Hickey, Erin; Peterson, Jeremy; Tettelin, Herve ; Venter, J. Craig; Masignani, Vega; Galeotti, Cesira;** Mora, Marirosa; **Ratti, Giulio; Scarselli, Maria; Scarlato, Vincenzo; Rappuoli, Rino; Pizza, Mariagratia**

PATENT ASSIGNEE(S): Chiron Corporation, USA

SOURCE: PCT Int. Appl., 1760 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 5

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000022430	A2	20000420	WO 1999-US23573	19991008
WO 2000022430	A3	20020606		
WO 2000022430	C2	20020704		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
NZ 527182	A	20040625	NZ 1999-527182	19990430
CA 2346713	AA	20000420	CA 1999-2346713	19991008
EP 1144998	A2	20011017	EP 1999-970470	19991008
EP 1144998	A3	20020807		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,				

PT, IE, SI, LT, LV, FI, RO

BR 9914374	A	20020917	BR 1999-14374	19991008
RU 2223492	C2	20040210	RU 2001-112411	19991008
JP 2004511201	T2	20040415	JP 2000-576277	19991008
NZ 511540	A	20040528	NZ 1999-511540	19991008
EP 1559795	A2	20050803	EP 2005-75407	19991008
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY				
CA 2371032	AA	20001109	CA 2000-2371032	20000308
WO 2000066791	A1	20001109	WO 2000-US5928	20000308
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1185691	A1	20020313	EP 2000-910392	20000308
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 2000010361	A	20030610	BR 2000-10361	20000308
JP 2003527079	T2	20030916	JP 2000-615413	20000308
RU 2233328	C2	20040727	RU 2001-132325	20000308
AU 780308	B2	20050317	AU 2000-32492	20000308

PRIORITY APPLN. INFO.:	US 1998-103794P	P	19981009
	US 1999-132068P	P	19990430
	US 1998-83758P	P	19980501
	US 1998-94869P	P	19980731
	US 1998-98994P	P	19980902
	US 1998-99062P	P	19980902
	US 1998-103749P	P	19981009
	US 1998-103796P	P	19981009
	US 1999-121528P	P	19990225
	EP 1999-970470	A3	19991008
	WO 1999-US23573	W	19991008
	GB 2000-4695	A	20000228
	WO 2000-US5928	W	20000308

AB The invention provides methods of obtaining immunogenic proteins from genomic sequences including Neisseria, including the amino acid sequences and the corresponding nucleotide sequences, as well as the complete genomic sequence and 931 contig sequences of **Neisseria meningitidis** serotype B. **Open reading frames** and predicted protein sequences are also provided and compared for **N. meningitidis**

serotype B, **N. meningitidis** A, and N. gonorrhoeae.
The proteins so obtained are useful antigens for vaccines, immunogenic compns., and/or diagnostics.

L39 ANSWER 17 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 6
ACCESSION NUMBER: 2000:181737 CAPLUS
DOCUMENT NUMBER: 133:38934
TITLE: Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
AUTHOR(S): **Pizza, Mariagrazia; Scarlato, Vincenzo; Masignani, Vega;** Giuliani, Marzia Monica; Arico, Beatrice; Comanducci, Maurizio; Jennings, Gary T.; Baldi, Lucia; Bartolini, Erika; Capecchi, Barbara; **Galeotti, Cesira L.**; Luzzi, Enrico; Manetti, Roberto; Marchetti, Elisa; Moray, Márirosa; Nuti, Sandra; **Ratti, Giulio;** Santini, Laura; Savino, Silvana; **Scarselli, Maria;** Storni, Elisa; Zuo, Peijun; Broeker, Michael; Hundt, Erika; Knapp, Bernard; Blair, Eric; Mason, Tanya; Tettelin, Herve; Hood, Derek W.; Jeffries, Alex C.; Saunders, Nigel J.; Granoff, Dan M.; **Venter, J. Craig;** Moxon, E. Richard; **Grandi, Guido; Rappuoli, Rino**
CORPORATE SOURCE: IRIS, Chiron S.p.A, Siena, D-35006, Italy
SOURCE: Science (Washington, D. C.) (2000), 287(5459), 1816-1820
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Neisseria meningitidis is a major cause of bacterial septicemia and meningitis. Sequence variation of surface-exposed proteins and cross-reactivity of the serogroup B capsular polysaccharide with human tissues have hampered efforts to develop a successful vaccine. To overcome these obstacles, the entire genome sequence of a virulent serogroup B strain (MC58) was used to identify vaccine candidates. A total of 350 candidate antigens were expressed in Escherichia coli, purified, and used to immunize mice. The sera allowed the identification of proteins that are surface exposed, that are conserved in sequence across a range of strains, and that induce a bactericidal antibody response, a property known to correlate with vaccine efficacy in humans.
REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 18 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 2000:181732 CAPLUS
DOCUMENT NUMBER: 132:203916
TITLE: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
AUTHOR(S): Tettelin, Herve; Saunders, Nigel J.; Heidelberg, John; Jeffries, Alex C.; Nelson, Karen E.; Eisen, Jonathan A.; Ketchum, Karen A.; Hood, Derek W.; Peden, John F.; Dodson, Robert J.; Nelson, William

C.; Gwinn, Michelle L.; DeBoy, Robert; Peterson, Jeremy D.; Hickey, Erin K.; Haft, Daniel H.; Salzberg, Steven L.; White, Owen; Fleischmann, Robert D.; Dougherty, Brian A.; Mason, Tanya; Ciecko, Anne; Parksey, Debbie S.; Blair, Eric; Cittone, Henry; Clark, Emily B.; Cotton, Matthew D.; Utterback, Terry R.; Khouri, Hoda; Qin, Haiying; Vamathevan, Jessica; Gill, John; **Scarlato, Vincenzo; Masignani, Vega; Pizza, Mariagrazia; Grandi, Guido;** Sun, Li; Smith, Hamilton O.; Fraser, Claire M.; Moxon, E. Richard; **Rappuoli, Rino; Venter, J. Craig**

CORPORATE SOURCE: The Institute for Genomic Research (TIGR), Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5459), 1809-1815
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The 2,272,351-bp genome of Neisseria meningitidis strain MC58 (serogroup B), a causative agent of meningitis and septicemia, contains 2158 predicted coding regions, 1158 (53.7%) of which were assigned a biol. role. Three major islands of horizontal DNA transfer were identified; two of these contain genes encoding proteins involved in pathogenicity, and the third island contains coding sequences only for hypothetical proteins. Insights into the commensal and virulence behavior of N. meningitidis can be gleaned from the genome, in which sequences for structural proteins of the pilus are clustered and several coding regions unique to serogroup B capsular polysaccharide synthesis can be identified. Finally, N. meningitidis contains more genes that undergo phase variation than any pathogen studied to date, a mechanism that controls their expression and contributes to the evasion of the host immune system.

REFERENCE COUNT: 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 19 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 8

ACCESSION NUMBER: 2000:557745 CAPLUS

DOCUMENT NUMBER: 134:26000

TITLE: Repeat-associated phase variable genes in the complete genome sequence of Neisseria meningitidis strain MC58

AUTHOR(S): Saunders, Nigel J.; Jeffries, Alex C.; Peden, John F.; Hood, Derek W.; **Tettelin, Herve; Rappuoli, Rino;** Moxon, E. Richard

CORPORATE SOURCE: The Molecular Infectious Disease Group, Institute of Molecular Medicine, University of Oxford, Oxford, OX3 9DS, UK

SOURCE: Molecular Microbiology (2000), 37(1), 207-215
CODEN: MOMIEE; ISSN: 0950-382X

PUBLISHER: Blackwell Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Phase variation, mediated through variation in the length of simple sequence repeats, is recognized as an important mechanism for

controlling the expression of factors involved in bacterial virulence. Phase variation is associated with most of the currently recognized virulence determinants of **Neisseria meningitidis**. Based upon the complete genome sequence of the **N. meningitidis** serogroup B strain MC58, we have identified tracts of potentially unstable simple sequence repeats and their potential functional significance determined on the basis of sequence context. Of the 65 potentially phase variable genes identified, only 13 were previously recognized. Comparison with the sequences from the other two pathogenic Neisseria sequencing projects shows differences in the length of the repeats in 36 of the 65 genes identified, including 25 of those not previously known to be phase variable. Six genes that did not have differences in the length of the repeat instead had polymorphisms such that the gene would not be expected to be phase variable in at least one of the other strains. A further 12 candidates did not have homologues in either of the other two genome sequences. The large proportion of these genes that are associated with frameshifts and with differences in repeat length between the neisserial genome sequences is further corroborative evidence that they are phase variable. The number of potentially phase variable genes is substantially greater than for any other species studied to date, and would allow **N. meningitidis** to generate a very large repertoire of phenotypes through expression of these genes in different combinations. Novel phase variable candidates identified in the strain MC58 genome sequence include a spectrum of genes encoding glycosyltransferases, toxin related products, and metabolic activities as well as several restriction/modification and bacteriocin-related genes and a number of **open reading frames** (**ORFs**) for which the function is currently unknown. This suggests that the potential role of phase variation in mediating bacterium-host interactions is much greater than has been appreciated to date. Anal. of the distribution of homopolymeric tract lengths indicates that this species has sequence-specific mutational biases that favor the instability of sequences associated with phase variation.

REFERENCE COUNT: 70 THERE ARE 70 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L39 ANSWER 20 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 9

ACCESSION NUMBER: 1999:723179 CAPLUS
DOCUMENT NUMBER: 131:335798
TITLE: Neisseria meningitidis and N. gonorrhoeae antigens and the genes encoding them for use as vaccine and diagnostic compositions
INVENTOR(S): Fraser, Claire; Galeotti, Cesira; Grandi, Guido; Hickey, Erin; Masignani, Vega; Mora, Marirosa; Petersen, Jeremy; Pizza, Mariagratia; Rappuoli, Rino; Ratti, Giulio; Scalato, Enzo; Scarselli, Maria; Tettelin, Herve; Venter, J. Craig
PATENT ASSIGNEE(S): Chiron Corporation, USA; The Institute for Genomic Research
SOURCE: PCT Int. Appl., 1453 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9957280	A2	20000824	WO 1999-US9346	19990430
WO 9957280	C2	20020829		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2330838	AA	19991111	CA 1999-2330838	19990430
AU 9939677	A1	19991123	AU 1999-39677	19990430
AU 761780	B2	20030612		
EP 1093517	A2	20010425	EP 1999-922752	19990430
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2004500801	T2	20040115	JP 2000-547235	19990430
NZ 508366	A	20040326	NZ 1999-508366	19990430
RU 2227043	C2	20040420	RU 2000-130221	19990430
BR 9910089	A	20040608	BR 1999-10089	19990430
NZ 527182	A	20040625	NZ 1999-527182	19990430
PRIORITY APPLN. INFO.:			US 1998-83758P	P 19980501
			US 1998-94869P	P 19980731
			US 1998-98994P	P 19980902
			US 1998-99062P	P 19980902
			US 1998-103749P	P 19981009
			US 1998-103796P	P 19981009
			US 1998-104794P	P 19981009
			US 1999-121528P	P 19990225
			US 1998-103794P	P 19981009
			WO 1999-US9346	W 19990430

AB The invention provides 1510 proteins from Neisseria meningitidis and N. gonorrhoeae, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics. Conservation of ORFs 225, 235, 287,419 and 919 is confirmed by sequencing of the proteins from multiple strains each. In addition, PCR primer pairs are provided for amplification of the open reading frames.

L39 ANSWER 21 OF 21 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 10
ACCESSION NUMBER: 1999:326052 CAPLUS
DOCUMENT NUMBER: 131:2733
TITLE: Candidate antigens of Neisseria and the genes encoding them and their diagnostic, prophylactic and therapeutic uses
INVENTOR(S): **Masignani, Vega; Rappuoli, Rino ; Pizza, Mariagrazia; Scarlato,**

Vincenzo; Grandi, Guido
PATENT ASSIGNEE(S): Chiron S.p.A., Italy
SOURCE: PCT Int. Appl., 524 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9924578	A2	19990520	WO 1998-IB1665	19981009
WO 9924578	A3	20000302		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2308606	AA	19990520	CA 1998-2308606	19981009
AU 9893637	A1	19990531	AU 1998-93637	19981009
EP 1029052	A2	20000823	EP 1998-946675	19981009
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003522514	T2	20030729	JP 2000-520572	19981009
RU 2232191	C2	20040710	RU 2000-114245	19981009
US 6914131	B1	20050705	US 1999-303518	19990430

PRIORITY APPLN. INFO.:	GB 1997-23516	A	19971106
	GB 1997-24190	A	19971114
	GB 1997-24386	A	19971118
	GB 1997-25158	A	19971127
	GB 1997-26147	A	19971210
	GB 1998-759	A	19980114
	GB 1998-19016	A	19980901
	WO 1998-IB1665	W	19981009

AB Proteins of **Neisseria meningitidis** (strains A and B) and Neisseria gonorrhoeae that may be useful as antigens in the diagnosis, prophylaxis, and treatment of meningitis and gonorrhea are described and genes encoding them are cloned and expressed in Escherichia coli. Cloning and expression of the genes or partial **open reading frames** using hexahistidine tags for affinity purification are described. Results from BLAST searches identifying possible homologs of many of the genes are reported.

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                OR MENINGOCOCC?)
L2            71 SEA ABB=ON  PLU=ON  L1(L)(IDENTIF? OR DETERM? OR DETECT?
                OR DET## OR SCREEN?)
L3            24 SEA ABB=ON  PLU=ON  L2(L)NUCLEOTIDE
                D KWIC
L4            22 SEA ABB=ON  PLU=ON  L3(L)(AMINO OR PROTEIN OR POLYPROTEIN
                OR PEPTIDE OR POLYPEPTIDE)
                D KWIC

     FILE 'CAPLUS' ENTERED AT 14:37:26 ON 15 AUG 2005
                D QUE
                D L4 1-22 .BEVERLY

     FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
     JICST-EPLUS, JAPIO' ENTERED AT 14:37:28 ON 15 AUG 2005
L5            81 SEA ABB=ON  PLU=ON  L4
L6            26 DUP REM L5 (55 DUPLICATES REMOVED)
                D 1-26 IBIB ABS

     FILE 'USPATFULL' ENTERED AT 14:42:39 ON 15 AUG 2005
L7           139 SEA ABB=ON  PLU=ON  (ORF OR OPEN READ? FRAME OR PROTEIN
                CODING SEQUENC?)(S)(NMB(S)(MENINGIT? OR MENINGOCOCC?) OR
                (NEISSER? OR N)(W)MENINGITID? OR MENINGOCOCC?)
L8            85 SEA ABB=ON  PLU=ON  L7(S)(IDENTIF? OR DETERM? OR DETECT?
                OR DET## OR SCREEN?)
L9            20 SEA ABB=ON  PLU=ON  L8(S)NUCLEOTIDE
L10           17 SEA ABB=ON  PLU=ON  L9(S)(AMINO OR PROTEIN OR POLYPROTEIN
                OR PEPTIDE OR POLYPEPTIDE)
                D QUE
                D 1-17 .BEVPAT

     FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
     JICST-EPLUS, JAPIO, USPATFULL' ENTERED AT 14:45:26 ON 15 AUG 2005
L11         4839 SEA ABB=ON  PLU=ON  "FRASER C"?/AU
L12          683 SEA ABB=ON  PLU=ON  "HICKEY E"?/AU
L13        12066 SEA ABB=ON  PLU=ON  "PETERSON J"?/AU
L14          199 SEA ABB=ON  PLU=ON  "TETTELIN H"?/AU
L15         2320 SEA ABB=ON  PLU=ON  ("VENTER C"? OR "VENTER J"?)/AU
L16          170 SEA ABB=ON  PLU=ON  "MASIGNANI V"?/AU
L17          167 SEA ABB=ON  PLU=ON  "GALEOTTI C"?/AU
L18          507 SEA ABB=ON  PLU=ON  "RATTI G"?/AU
L19          304 SEA ABB=ON  PLU=ON  "SCARSELLI M"?/AU
L20          326 SEA ABB=ON  PLU=ON  "SCARLATO V"?/AU
L21         2315 SEA ABB=ON  PLU=ON  "RAPPUOLI R"?/AU
L22          625 SEA ABB=ON  PLU=ON  "PIZZA M"?/AU
L23          914 SEA ABB=ON  PLU=ON  "GRANDI G"?/AU
L24            2 SEA ABB=ON  PLU=ON  L11 AND L12 AND L13 AND L14 AND L15
                AND L16 AND L17 AND L18 AND L19 AND L20 AND L21 AND L22
                AND L23
L25          870 SEA ABB=ON  PLU=ON  L11 AND (L12 OR L13 OR L14 OR L15 OR
                L16 OR L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23)
L26           92 SEA ABB=ON  PLU=ON  L12 AND (L13 OR L14 OR L15 OR L16 OR
                L17 OR L18 OR L19 OR L20 OR L21 OR L22 OR L23)
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Searcher : Shears 571-272-2528

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L27         114 SEA ABB=ON  PLU=ON  L13 AND (L14 OR L15 OR L16 OR L17 OR
                L18 OR L19 OR L20 OR L21 OR L22 OR L23)
L28          86 SEA ABB=ON  PLU=ON  L14 AND (L15 OR L16 OR L17 OR L18 OR
                L19 OR L20 OR L21 OR L22 OR L23)
L29          16 SEA ABB=ON  PLU=ON  L15 AND (L16 OR L17 OR L18 OR L19 OR
                L20 OR L21 OR L22 OR L23)
L30         155 SEA ABB=ON  PLU=ON  L16 AND (L17 OR L18 OR L19 OR L20 OR
                L21 OR L22 OR L23)
L31          37 SEA ABB=ON  PLU=ON  L17 AND (L18 OR L19 OR L20 OR L21 OR
                L22 OR L23)
L32         121 SEA ABB=ON  PLU=ON  L18 AND (L19 OR L20 OR L21 OR L22 OR
                L23)
L33          77 SEA ABB=ON  PLU=ON  L19 AND (L20 OR L21 OR L22 OR L23)
L34         214 SEA ABB=ON  PLU=ON  L20 AND (L21 OR L22 OR L23)
L35         611 SEA ABB=ON  PLU=ON  L21 AND (L22 OR L23)
L36          50 SEA ABB=ON  PLU=ON  L22 AND L23
L37          32 SEA ABB=ON  PLU=ON  (L25 OR L26 OR L27 OR L28 OR L30 OR
                L31 OR L32 OR L33 OR L34 OR L35 OR L36) AND L1
L38          43 SEA ABB=ON  PLU=ON  L24 OR L29 OR L37
L39          21 DUP REM L38 (22 DUPLICATES REMOVED)
                D 1-21 IBIB ABS

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 RLOAD at an arrow promt (=>).  See also:

    http://www.nlm.nih.gov/mesh/
    http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html

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 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
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MeSH 2005 vocabulary.

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FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 4 August 2005 (20050804/ED)

FILE RELOADED: 19 October 2003.

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FILE COVERS 1973 TO 25 May 2005 (20050525/ED)

FILE SCISEARCH

FILE COVERS 1974 TO 11 Aug 2005 (20050811/ED)

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FILE COVERS 1985 TO 8 AUG 2005 (20050808/ED)

THE JICST-EPLUS FILE HAS BEEN RELOADED TO REFLECT THE 1999 CONTROLLED TERM (/CT) THESAURUS RELOAD.

FILE JAPIO
FILE LAST UPDATED: 2 AUG 2005 <20050802/UP>
FILE COVERS APR 1973 TO APRIL 28, 2005

<<< GRAPHIC IMAGES AVAILABLE >>>

FILE USPATFULL
FILE COVERS 1971 TO PATENT PUBLICATION DATE: 11 Aug 2005 (20050811/PD)
FILE LAST UPDATED: 11 Aug 2005 (20050811/ED)
HIGHEST GRANTED PATENT NUMBER: US6928656
HIGHEST APPLICATION PUBLICATION NUMBER: US2005177917
CA INDEXING IS CURRENT THROUGH 11 Aug 2005 (20050811/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 11 Aug 2005 (20050811/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Jun 2005
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